sequence 5, Appli Sequence 16, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 3, Appli Sequence 3, Appli Sequence 4, Appli Sequence 4, Appli Sequence 1, Appli Sequence 1, Appli Sequence 36, Appli Sequence 36, Appli Sequence 1, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 5, Appli

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Word size :

Searched:

Database :

Scoring table:

Perfect score:

Sequence:

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on:

Run

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US-LO-US-SB-1

SGRUERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Kingsman, Alan J.

APPLICANT: Bebbington, Christopher R.

APPLICANT: Ellard, Fiona M.

APPLICANT: Kingsman, Susan M.

APPLICANT: Myers, Kevin A.

TITLE REFERRNCE: DYOUZ: 0010CP1

CURRENT FILING DATE: 1090-06

PRIOR PILING DATE: 1998-06-04

PRIOR FILING DATE: 1999-06-04

PRIOR FILING DATE: 1999-06-04

PRIOR FILING DATE: 1997-06-04

PRIOR FILING DATE: 1997-06-04

PRIOR PILING DATE: 1997-06-20

PRIOR PILING DATE: 1997-06-20

PRIOR PILING DATE: 1997-06-20

PRIOR PILING DATE: 1997-07-04

PRIOR PILING DATE: 1997-07-04

PRIOR PILING DATE: 1999-11-13

PRIOR PILING DATE: 1999-11-13

PRIOR PILING DATE: 1999-11-13

PRIOR PILING DATE: 1999-11-13

PRIOR PILING DATE: 1999-11-18

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FASLESQ for Windows Version 4.0

SEQ ID NO 1

LENGTH: 729

TYPE: DNA

ORGANISM: Artificial Sequence
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   4444000000000000000
  US-10-060-585-1
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                                                                                      March 15, 2005, 22:23:06 ; Search time 611 Seconds
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Sequence 2,
Sequence 2,
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| cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NWW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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7: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
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12: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-787-881A-1
US-10-060-585-2
US-10-334-235-2
US-10-787-881A-2
US-10-787-881A-2
US-10-334-235-3
US-10-334-235-3
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                                                                - nucleic search, using sw model
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Gapop_60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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COTHER INFORMATION: DNA encoding a 5T4 scFv,
US-10-334-235-1
                                                                                                                                                                                                                                                                                                             100.0%; Score 729; D
100.0%; Pred. No. 0;
ive 0; Mismatches
        CURRENT APPLICATION NUMBER: US/10/334,235
CURRENT FILING DATE: 2002-12-30
FRIOR APPLICATION NUMBER: US/10/60,585
FRIOR APPLICATION NUMBER: US 10/60,585
FRIOR APPLICATION NUMBER: US 10/60,585
FRIOR PILING DATE: 2002-01-29
FRIOR PILING DATE: 2000-11-13
FRIOR FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 40
SEQ ID NO 1
LENGTH: 729
TITLE OF INVENTION: VECTOR SYSTEM
                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.
Matches 729; Conservative
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                                             DB 14;
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                                           ; Score 729; DB
; Pred. No. 0;
0; Mismatches
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Publication No. US20040131591A1
GENERAL INFORMATION:
APPLICANT: Oxfard Blomedica (UK) Ltd.
APPLICANT: Kingsman, Alan
APPLICANT: Elbard, Flona
APPLICANT: Ellard, Flona
APPLICANT: Kingsman, Susan
APPLICANT: Kingsman, Susan
APPLICANT: Kingsman, Susan
APPLICANT: Lamikandan, Abigail
                                             100.0%;
; OTHER INFORMATION: 5T4 SCFV
US-10-060-585-1
                                           Query Match 100.
Best Local Similarity 100.
Matches 729; Conservative
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CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT
                                    541 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT
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US-10-060-585-2

Sequence 2, Application US/10060585

Publication No. US20030083290A1

GENERAL INFORMATION:

APPLICANT: Kingsman, Alan J.

APPLICANT: Ellard, Fiona M.

APPLICANT: BOUCTON SYSTEM

FILE REFERENCE: DYOUZ3.001CP1

CURRENT APPLICATION NUMBER: US 09/46375

PRIOR FILING DATE: 1997-06-04

PRIOR APPLICATION NUMBER: GB 9713150.2

PRIOR FILING DATE: 1997-06-04

PRIOR FILING DATE: 1997-06-04

PRIOR FILING DATE: 1997-06-04

PRIOR FILING DATE: 1997-07-04

PRIOR FILING DATE: 1997-07-04

PRIOR PRIING DATE: 1997-07-04

PRIOR FILING DATE: 1997-01-13

PRIOR FILING DATE: 1997-11-13

PRIOR FILING DATE: 2000-11-13

PRIOR FILING DATE: 2000-11-13

PRIOR FILING DATE: 2000-11-13

PRIOR FILING DATE: 1909-11-18

NUMBER OF SEQ ID NOS: 27

SSQITWARE: FastESQ for Windows Version 4.0

SSQITWARE: 1007-10-13
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; OTHER INFORMATION: 5T4Sab1
US-10-060-585-2
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COTHER INFORMATION: Coding sequence of 5T4scFv
US-10-787-881A-1
                                                                                                                                                                                                                     APPLICANT: Oxford BioMedica (UK) Ltd.
APPLICANT: Kingsman, Susan M.
APPLICANT: Kingsman, Susan M.
APPLICANT: Babbington, Christopher R.
APPLICANT: Bland, Fiona M.
APPLICANT: Carroll, Miles M.
APPLICANT: Carroll, Miles W.
TITLE OP INVENTION: Vector
FILE REFERENCE: 021911-000330US
CURRENT APPLICATION NUMBER: US/10/787,881A
CURRENT FILING DATE: 2004-02-25
PRIOR APPLICATION NUMBER: US 9/445,375
PRIOR APPLICATION NUMBER: PCT/GB98/01627
PRIOR APPLICATION NUMBER: PCT/GB98/01627
PRIOR APPLICATION NUMBER: PCT/GB98/01627
PRIOR APPLICATION NUMBER: PCT/GB98/01627
PRIOR SPLING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 24
NUMBER OF SEQ ID NOS: 24
                                                                                                                                                ; Sequence 1, Application US/10787881A; Publication No. US20050012216A1; GENERAL INFORMATION:
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US-10-334-235-2
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APPLICANT: Kingeman, Alan
APPLICANT: Bebbington, Christopher
APPLICANT: Ellard, Flona
APPLICANT: Ellard, Flona
APPLICANT: Kingeman, Susan
APPLICANT: Kingeman, Susan
APPLICANT: Kingeman, Susan
APPLICANT: Lamikandra, Abigail
TITLE OF INVENTION: VETTOR SYSTEM
TITLE OF INVENTION: VETTOR SYSTEM
TITLE OF INVENTION NUMBER: US/10/334,235
CURRENT APPLICATION NUMBER: US/10/60,585
PRIOR FILING DATE: 2000-11-29
PRIOR FILING DATE: 2000-11-39
PRIOR FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 40
SEQ ID NOS: 40
SEQ ID NOS: 40
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APPLICANT: Kingsman, Susan M.
APPLICANT: Kingsman, Susan M.
APPLICANT: Blabbington, Christopher R.
APPLICANT: Eladd, Fiona M.
APPLICANT: Carroll, Miles W.
APPLICANT: Myers, Kevin A.
TITLE REPERENCE: 021911-000330US
FILE REFERENCE: 021911-000330US
CURRENT APPLICATION NUMBER: US/10/767,881A
CURRENT APPLICATION NUMBER: US 09/445,375
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR PELLING DATE: 2000-03-21
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; OTHER INFORMATION: Sequence encoding 5T4 single chain antibody
US-10-787-881A-2
                                                                                                                                   Score 678; DB 19; Length 1807;
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US-10-060-585-3
Sequence 3, Application US/10060585; Publication No. US20030083290A1
GENERAL INFORMATION:
                                                                                                                                    93.0%;
99.9%;
PRIOR FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
                                                            TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                   Query Match
Best Local Similarity 99.94
Matches 728; Conservative
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APPLICANT: Kingsman, Alan J.
APPLICANT: Bebbington, Christopher R.
APPLICANT: Carroll, Miles W.
APPLICANT: Ellard, Fiona M.
APPLICANT: Ellard, Fiona M.
APPLICANT: Kingsman, Susan M.
APPLICANT: Wyers, Kevin A.
TILE OF INVENTION: VECTOR SYSTEM
FILE REFERENCE: DYOUZ3.001CP1
CURRENT APPLICATION NUMBER: US/10/060,585
PRIOR APPLICATION NUMBER: US 09/445375
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1999-06-04
PRIOR FILING DATE: 1997-06-04
PRIOR FILING DATE: 1997-06-04
PRIOR FILING DATE: 1997-06-04
PRIOR FILING DATE: 1997-06-04
PRIOR FILING DATE: 1997-07-09
PRIOR FILING DATE: 1997-07-09
PRIOR FILING DATE: 1997-07-04
PRIOR FILING DATE: 1997-07-04
PRIOR FILING DATE: 1999-01-13
PRIOR FILING DATE: 1999-11-13
PRIOR FILING DATE: 1999-11-13
PRIOR FILING DATE: 1999-11-13
PRIOR FILING DATE: 2000-11-13
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US-10-060-585-3
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1219 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1278
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                                                      1039 ATGATTACGAACTATGTTATGGACTACTGGGGGTCAAGTAACCTCAGTCACGGCCTCCTCA 1098
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                  301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
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; OTHER INFORMATION: Sequence encoding fusion protein B7-1.5T4.1 US-10-787-881A-3
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APPLICANT: Kingsman, Susan M.
APPLICANT: Kingsman, Susan M.
APPLICANT: Blabbington, Christopher R.
APPLICANT: Blatd, Fiona M.
APPLICANT: Carroll, Miles W.
APPLICANT: Carroll, Miles W.
TITLE OF INVENTION: Vector
TITLE REFERENCE: 021911-000330US
CURRENT APPLICATION NUMBER: US/10/787,881A
CURRENT FILING DATE: 2004-02-25
PRIOR APPLICATION NUMBER: US 99/445,375
PRIOR APPLICATION NUMBER: US 09/445,375
PRIOR APPLICATION NUMBER: PCT/GB98/01627
PRIOR PILING DATE: 1998-06-04
NUMBER OF SEO ID NOS: 24
SOFTWARE: PatentIn version 3.1
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ORGANISM: Artificial Sequence
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LENGTH: 1467
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1399 TATTICTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1458
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APPLICANT: Kingsman, Alan
APPLICANT: Bebbington, Christopher
APPLICANT: Elazd, Fiona
APPLICANT: Elazd, Fiona
APPLICANT: Kingsman, Susan
APPLICANT: Kingsman, Susan
APPLICANT: Kingsman, Susan
APPLICANT: Myers, Kevin
TITLE OF INVENTION: VECTOR SYSTEM
FILE REFERENCE: 53262000920
CURRENT PEPLICATION NUMBER: US/10/334,235
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: PCT/GB00/04317
PRIOR FILING DATE: 2000-11-13
PRIOR FILING DATE: 2000-11-13
PRIOR FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PSELSEQ for Windows Version 4.0
SEG ID NO: 11467
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Publication No. US20040131591A1
Publication No. WS20040131591A1
APPLICANT: Oxfard Biomedica (UK) Ltd.
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ORGANISM: Artificial Sequence
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TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Publication No. US2030018004A1

GENERAL INFORMATION:
APPLICANT: Ringsman, Susan M.
APPLICANT: Bland, Fiona M.
TITLE OF INVENTION: VECTOR
TITLE OF INVENTION: VECTOR
FILE REFERENCE: DYOUZ3.001DV1
CURRENT APPLICATION NUMBER: 09/445375
FRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/445375
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1997-06-04
PRIOR FILING DATE: 1997-06-04
PRIOR FILING DATE: 1997-06-04
PRIOR PRILING DATE: 1997-06-20
PRIOR PRILING DATE: 1997-06-20
PRIOR PRILING DATE: 1997-06-20
PRIOR PRILING DATE: 1997-07-04
NUMBER: OF SEQ ID NOS: 24
SEQ ID NO 5
LENGTH: 1518
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                                                                        DB 14; Length 1518;
                                                                                                                 3; Indels
                                                                   Ouery Match 79.0%; Score 576; DB 14 Best Local Similarity 99.6%; Pred. No. 6e-294; Matches 726; Conservative 0; Mismatches
; OTHER INFORMATION: pBSII/Leader/scFv/HG1
US-10-104-522-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kingsman, Alan
APPLICANT: Babbington, Christopher
APPLICANT: Barbington, Christopher
APPLICANT: Bland, Fiona
APPLICANT: Kingsman, Susan
APPLICANT: Kingsman, Susan
APPLICANT: Kingsman, Susan
APPLICANT: Lamikandra, Abigail
ITILE OF INVENTION: VECTOR SYSTEM
ITILE OF INVENTION: VECTOR SYSTEM
CURRENT APPLICATION NUMBER: US/10/334,235
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: US 10/060,585
PRIOR APPLICATION NUMBER: US 10/060,585
PRIOR PILING DATE: 2000-11-13
PRIOR PILING DATE: 2000-11-13
PRIOR PILING DATE: 2000-11-13
PRIOR PILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 40
SUMBER OF SEQ ID NOS: 40
SUPPLIANT: LAND NOS: 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Oxfard Biomedica (UK) Ltd. APPLICANT: Kingsman, Alan APPLICANT: Bebbington, Christopher APPLICANT: Carroll, Miles
                                                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/10334235 Publication No. US20040131591A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 726; Conserv
                                                                                                                                                                                                                                                                                                     RESULT 12
US-10-334-235-5
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Pred. No. 6e-294;
0; Mismatches 3;
                                                                                                                            PRIOR APPLICATION NUMBER: US 09/445375
PRIOR PELING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: US 09/445375
PRIOR APPLICATION NUMBER: GB 9711579.4
PRIOR APPLICATION NUMBER: GB 971350.2
PRIOR PELING DATE: 1997-06-20
PRIOR PELING DATE: 1997-06-20
PRIOR PELING DATE: 1997-06-10
PRIOR APPLICATION NUMBER: GB 9714230.1
PRIOR APPLICATION NUMBER: PCT/GB00/04317
PRIOR APPLICATION NUMBER: PCT/GB99/03859
PRIOR PLING DATE: 2000-11-13
PRIOR PLING DATE: 1999-11-18
PRIOR PLING DATE: 1999-11-18
PRIOR PLING DATE: 1999-11-18
PRIOR PLING DATE: 1999-11-18
PRIOR PLING DATE: PCT/GB99/03859
APPLICANT: Myers, Kevin A.
TITLE OF INVENTION: VECTOR SYSTEM
TILE REFERENCE: DYOUZ3.001CPI
CURRENT APPLICATION NUMBER: US/10/060,585
CURRENT FILING DATE: 2002-09-06
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CTHER INFORMATION: B7 link ScFv sequence
US-10-060-585-5
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ORGANISM: Artificial Sequence
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Best Local Similarity 99.6
Matches 726; Conservative
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OTHER INFORMATION: nuc sequence of the SMART2 LscFvB7.1 5' CPPT
OTHER INFORMATION: plasmid
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APPLICANT: Kingaman, Alan
APPLICANT: Carroll, Miles
APPLICANT: Elard, Fiona
APPLICANT: Elard, Fiona
APPLICANT: Kingaman, Susan
APPLICANT: Kingaman, Susan
APPLICANT: Kingaman, Susan
APPLICANT: Kingaman, Susan
APPLICANT: Lamkkandra, Abigail
TITLE OF INVENTION: VECTOR SYSTEM
FILE REFERENCE: 532682000920
CURRENT APPLICATION NUMBER: US/10/334,235
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: PCT/GB00/04317
PRIOR FILING DATE: 2000-11-13
PRIOR PLING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
LENGTH: 9100
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ORGANISM: Artificial Sequence
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79.0%; Score 576; DB 19;
Best Local Similarity 99.6%; Pred. No. 6e-294;
Matches 726; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Sequence encoding B7 Link scFv
US-10-787-881A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Oxford BioMedica (UK) Ltd.
APPLICANT: Kingsman, Susan M.
APPLICANT: Elbard, Flona M.
APPLICANT: Blard, Flona M.
APPLICANT: Garroll, Miles W.
APPLICANT: Garroll, Miles W.
TITLE OF INVENTION: Vector
FILE OF INVENTION: Vector
FILE OF INVENTION: Vector
FILE OF INVENTION NUMBER: US/10/787, 881A
CURRENT APPLICATION NUMBER: US 09/445,375
PRIOR FILING DATE: 2000-02-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Version 3.1
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US-10-787-881A-5
Sequence 5, Application US/10787881A
; Publication No. US20050032216A1
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Best Local Similarity 99.6%; Pred. No. 1e-280;
Matches 701; Conservative 0; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: 5T4 scFV-human IgE fusion construct.
US-10-104-522-6
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION UNMBER: PCT/GB98/01627
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1997-06-00
PRIOR PLING DATE: 1997-06-20
PRIOR PLING DATE: 1997-06-20
PRIOR APPLICATION NUMBER: GB9713150.2
PRIOR PLING DATE: 1997-06-20
PRIOR PLING DATE: 1997-06-20
PRIOR PLING DATE: 1997-07-04
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PSELSEQ for Windows Version 4.0
SCACID LO NOS: 24
LENGTH: 2090
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ORGANISM: Artificial Sequence
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                                       Length 9100;
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                                   Query Match 78.1%; Score 569; DB 18; Best Local Similarity 99.6%; Pred. No. 2.9e-290; Matches 719; Conservative 0; Mismatches 3;
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US-10-104-522-6
| Sequence 6, Application US/10104522
| Publication No. US20030018004A1
| GENERAL INFORMATION:
| APPLICANT: Kingsman, Susan M. |
| APPLICANT: Bebbington, C.R. |
| APPLICANT: Bland, Fiona M. |
| APPLICANT: Carroll, Miles W. |
| TITLE OF INVENTION: VECTOR |
| FILE REFERENCE: DYQU33.001DV1 |
| CURRENT APPLICATION NUMBER: US/10/104,522 |
| CURRENT APPLICATION NUMBER: 09/445375
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Job time : 615 secs

Perfect score:

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Searched:

Minimum DB @ Maximum DB @

Database

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BX969451 Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone WHPN79016, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Butheria; Rodentia; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases I to 842)
Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L.,
Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y.,
Rogers, J. and Bradley, A.
Direct Submission
Submitted (20-FBB-2004) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. http://www.sanger.ac.uk/MICER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BF168514 10-CGAP_Lu29 Mus musculus cDNA clone IMAGE:4017075 5', BF168514
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BY707828
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                                                                                                                                                                                                                                                                                                                            BX969451.1 GI:49700874
GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
Mus musculus
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/organiem="Mus musculus"
/mol_type="genomic DNA"
/db xref="taxon:10090"
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                                                                                                                                                                                                                                      ALIGNMENTS
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BY194132
BY117980
BY119951
CA577443
                                                                      BE371136
BY707828
                                        CA578968
CA580316
 BX969451
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RPCI-24-3
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K0622H02-
K0722B03-
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                                                                   March 15, 2005, 20:38:45; Search time 3427 Seconds (without alignments) 8097.126 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                 1 gaggtccagcttcagcagtc......ccaagctggaaatcaaacgg
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AZ610015
BH121432
BY346210
CA577954
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BQ1259014

BQ1263124

CR0263124

BR150371

BUJ46353

AK077918

BX980485

CA578116

CA578116

CA5781323

CA578323
           5.1.6
Compugen Ltd.
                                                                                                                                                                                   34239544 seqs, 19032134700 residues
                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
           version 5
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                                                  nucleic search, using sw model
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BE309592
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CA578116
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CA578323
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Gapop_60.0 , Gapext 60.0
          GenCore
Copyright (c) 1993
                                                                                                                                                                                                                                              seq length: 0
seq length: 200000000
                                                                                                            US-10-016-686-5
                                                                                                                                                                                                                                                                                                          9b est1:

9b htc: 3

9b est43: 3

9b est44: 3

9b est6: 3

9b 9s81: 3

9b 9s82: 3
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BF015548
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                                                                                                                                                                                      Context: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be http://image.llni.gov
Plate: LLAM9265 row: h column: 04
High quality sequence stop: 661.
                                                          Mus musculus
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
1 (bases 1 to 724)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="IMAGB:4017075"
/tiseuc type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH108"
/clone lib="NCI CGAP_Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: Sal1;
Site 2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 769)
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                                                                                                                            NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
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100.0%; Pred. No. 2.2e-34;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="CZECH II"
                                        Mus musculus (house mouse)
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Mus musculus
    GI:11048866
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Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF015548 507 bp mRNA linear EST 29-DEC-2000 uy23a08.yl NCI CGAP Lu30 Mus musculus cDNA clone IWAGE:3660374 5' similar to SW:HV14 WOUSE P01758 IG HEAVY CHAIN V REGION 108A PRECURSOR. ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                          /tissue type="gontaneous tumor, metastatic to mammary.
Stem call origin."
/lab_host="DHIOB"
/clone lib="NCI CGAP Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall;
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall;
Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
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Mus maculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukamalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (bases 1 to 507)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Clone distribution: MGC clone distribution information can be
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                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM9265 row: k column: 04
High quality sequence stop: 678.
Location/Qualifiers
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High quality sequence stop: 456.
Location/Qualifiers
1. :507
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/mol type="mRNA"
/strain="CZECH II"
/db xref="taxon:1009"
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                                                                                                                                                                                                                   /organism="Mus musculus"
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                                                                                                                                                                                                                                             /mol_type="mRNA"
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/db_xref="taxon:10090"
/clone="IMAGE:4017147"
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BF015548.1 GI:10746880
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86; Conservative
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Local Similarity
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BF580610
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Rukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
B. (Dases I to 594)
S. I (Dases I to 594)
I. (Dases I to 594)
L. Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Llocation/Qualifiers
Llocation/Qualifiers
/tissue_type="tumor, metastatic to mammary"
/lab host="DH108"
/clone_lib="NCI_CGAP_Lu30"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; transgenic model WNT-1, expression driven by
MTV-LIR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
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                                                                                                                                                                                                                                                                                                            83 CATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGGCCTTGAGTGGA
                                                                                                                                                                                                                                                Gaps
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0
                                                                                                                                                                                                    h 9.1%; Score 66; DB 2; Length 507; Similarity 100.0%; Pred. No. 1.2e-23; 66; Conservative 0; Mismatches 0; Indels
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/dev_stage="7 months"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/mtsfan="mix PVB/N, C57BL/6J"
/db xref="taxon:10090"
/clone="IMAGE:3489635"
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Matches 61; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                        234 TTGGAC 239
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                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                             Local
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KEYWORDS
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ORGANISM
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AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                Matches
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BE309592
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Gaps . 0 445 TCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTA 504

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brbs0610 883 bp mRNA linear EST 12-DEC-2000 602093730F1 NCI_CGAP_C024 Mus musculus cDNA clone IMAGE:4208022 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSS 24-JAN-2001
Mustayota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (Dases I to 1081)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

Email: Cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              110 rchachachachachthachthachthachachachachachachtharanna 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       445 TCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution: MGC clone distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZ706203

RPCI-23-236G24.TJ RPCI-23 Mus musculus genomic clone RPCI-23-236G24, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 883;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM9771 row: 1 column: 07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.4%; Score 61; DB 2; L6
100.0%; Pred. No. 6.3e-21;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 639 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                               BF580610.1 GI:11654322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ706203
AZ706203.1 GI:12433429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .883
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VERSION
KEYWORDS
SOURCE
ORGANISM
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E., SLC,

us-10-016-686-5.01i.rst

TITLE JOURNAL

COMMENT

REFERENCE AUTHORS

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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pWaPA2 (gql #4732114 [gb] AR125072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli X110-GGld (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AMONISMULS 635 bp DNA linear GSS 13-DEC-2000 LM0435N01F Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0435N01 F, genomic survey sequence.
AZ610015
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Mus musculus
Mus musculus
Mus musculus
Mus musculus
Muscare, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 635)
Munn, D., Aoyagi, A., Marber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Menen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Musce whole genome scaffolding with paired end reads from 10kb
plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="B. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone_llb="Mouse_lokb plasmid UGCIM library"
/note="Vector: PWD4Znr; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 CTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGATTGGAC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University of Utah Genome Center
University of Utah
Rm. 300, Biomedical Polymers Research Bldg., 20 S. 2030
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.7%; Score 56; DB 8; Length 348; 100.0%; Pred. No. 2.8e-18; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                      Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                          Seg primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 348.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10090"
/clone="UUGC1M0438F15"
                                                                                                                                                                                                                                                                                                                                                Plate: 0438 row: F column: 15
                                                                                                                                                                                                                                                       Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Err
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Robert B. Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ610015.1 GI:11732205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sex="Male"
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                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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Matches 5
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COMMENT
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AZ610015
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab host="DHIOB"
/clone lib="RPCI-23"
/clone lib="RPCI-2"
/clone lib="RPCI-2"
/clone lib="RPCI-2"
/clone lib="RPCI-2"
/clone lib="RPCI-2"
/clone lib="RPCI-2"
/clone lib="RPCI-3"
/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enail: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
Ibhary availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 236 row: G column: 24
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                   Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S.,
Akinret, B., Levins, M., Mcgann, S., Teegaye, G., Geer, K., Krol, M., de
Jong, P. and Fraser, C.M.
    Chordata, Craniata, Vertebrata, Buteleostomi, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Butheria; Rodentia; Sciurognathi; Muridae, Murinae, Mus. 1 (bases 1 to 348)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R., Tingey, A., von Niederhausern, A. and Wright, D., Weise, R. Duval, B. Weise, R. Stoker, C. Contact: Robert B. Weise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 AGATATCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     602 AGATATCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAG 544
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                                                                                                                                                                                                                             Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Unpublished (1999)
Other GSSB: RPCI-23-236G24.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 638;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.1%; Score 59; DB 8; Le
llarity 100.0%; Pred. No. 7.3e-20;
Conservative 0; Mismatches 0;

    .638
    /organism="Mus musculus"

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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="taxon:10090"
clone="RPCI-23-236G24"
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Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sex="Female"
Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 638)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
nes 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSS.
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LOCUS DEFINITION

RESULT 8 AZ611733

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

Matches

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ORIGIN

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FEATURES

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BY346210
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwD42 (gill4gplAR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     784 bp DNA linear GSS 19-JUL-2001
RPCI-24-300D2.TV RPCI-24 Mus musculus genomic clone RPCI-24-300D2,
genomic survey sequence.
                                                      Б
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 78).
Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M.,
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E.,
Russell, D., de Jong, P. and Fraser, C.M.
Whouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other GSSs: RPCI-24-30002.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="E. Coli strain XLIO-Gold, Tl-resistant, F-"
/clone llb="Mouse 10kb plasmid UTGCIM library"
/note="Vector: PWD42ry; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
                                                      Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTACTACATGCACTGGAGCAGAGCCATGGAAAGAGCCTTGAGTGGATTGGAC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.7%; Score 56; DB 8; Length 635
100.0%; Pred. No. 3e-18;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory Mouse DNA Resource
                                                                                                                                                                               Std Error: 0.00
                                                                                                                                                                                                    Plate: 0435 row: N column: 01
Seq primer: CGTTGTAAAACGACGCCAGT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                               High quality sequence stop: 635.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                    'db_xref="taxon:10090"
'clone="UUGC1M0435N01"
                                                                                                                                                       Email: ddunn@genetics.utah.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
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                                                                                                                                                                               Insert Length: 10000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                     Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                 .635
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Best Local Similarity
Matches 56; Conserv
                                    761.
308, b.
USA
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BH121432
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JOURNAL
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DRIGIN

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mus musculus

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

(Stazaki,Y.; Furuno,M.; Kasukawa,T.; Adachi,J.; Bono,H.; Kondo,S.; Nikaido,I.; Osato,N.; Saito,R.; Suzuki,H.; Yamanaka,I.; Kayosawa,H.; Yagi,K.; Tomaru,Y.; Hasegawa,Y.; Mogami,A.; Schombach,C.; Gojobori,T.; Paldarelli,R.; Hill,D.P.; Bult,C.; Hume,D.A.; Quackenbush,J.; Schriml,L.M.; Kanapin,A.; Matsuda,H.; Batalov,S.; Beisel,K.W.; Blake,J.A.; Bradt,D.; Brusic,V.; Chothia,C.; Corbani,L.B.; Cousins,S.; Dalla,B.; Dragani,T.A.; Fletcher,C.F.; Forrest,A.; Frazer,K.S.; Gaasterland,T.; Gariboldi,M.; Gissi,C.; Godzik,A.; Gough,J.; Grimmond,S.; Gustincich,S.; Hirokawa,N.; Jackson,I.J.; Jarvis,B.D.; Kanai,A.; Kawaji,H.; Kawasawa,Y.; Kedzierski,R.M.; King,B.L.; Konagaya,A.; Kawaji,H.; Martchionni,L.; McKenzie,L.; Miki,H.; Nagashima,T.; Numata,K.; Okido,T.; Pevila,B.; Long, Pesole,G.; Randchandran,S.; Ravasi,T.; Reed,J.; C.; Reed,D.J.; Reid,J.; Ringwald,M.; Sandelin,A.; Schneider,C.; Semple,C.A.; Setou,M.; Shimada,K.; Sandelin,A.; Schneider,C.; Wang,Y.; Watanaba,Y.; Wang,I.; Vana,Z.; Zavolan,M.; Zimmer,A.; Carninci,P.; Vang,I.; Yang,L.; Yuan,Z.; Zavolan,M.; Zimmer,A.; Carninci,P.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY346210
BY346210 RIKEN full-length enriched, whole joints Mus musculus CDNA
                                                                                                                                    Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-24. For BAC
Library availability, please contact Pieter de Jong
(pdejong@mail.cho.org). Clones may be purchased from BACPAC
Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 300 row: D column: 2
Seg primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Spleen/Brain"
/clone_lib="RFCI-24"
/note="Vector: pTARBAC1; Site 1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamH1 sites using MboI partially digested male CS7BL/6J DNA."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          452 TACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGCCTTGAGTGGATTGGAC 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 784;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
The Institute for Genomic Research 9712 Wedical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7.1%; Score 52; DB 8; Le
100.0%; Pred. No. 4.3e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.1%; Score 52; DB Best Local Similarity 100.0%; Pred. No. 4.3 Matches 52; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone L730022G23 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .784
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-24-300D2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Mus musculus
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JOURNAL MEDLINE

TITLE

PUBMED

COMMENT

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/clone lib="NIA Mouse Hematopoietic Stem Cell
(lin-/c-Kit-/Sca-1-) CDNA Library (Long)"
(note="Vector: pSPORT! (Invitrogen); Site_1: Sall; Site_2:
Not!; Mouse CDNA project by the Laboratory of Genetics,
Notional Institute on Aging (NIA), Intramural Research
Program, NIH (http://lgsun.grc.nia.nih.gov/CDNA). This is
a long-transcript enriched CDNA library (Ref. Genome Res.
11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were
obtained from Drs. Dennis Taub, Dan Longo (National
Institute on Aging, USA), Jonathan Keller (National
Institute, USA). Double-stranded cDNAs were suith an Oligo(dT) primer [Invitrogen:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                            1 (bases 1 to 529)
Piao, Y., Kargul, G.J., Dudekula, D.B., Qian, Y., Luo, A., Carter, M.G., Aiba, K., Taub, D., Longo, D.L., Keller, J. and Ko, M.S.H.
Systematic Analyses of NIA Mouse Hematopoletic Stem Cell
                                                                                                                                                                                                                                                                                                                                                  Unpublished (2001)
Other ESTS: K0716F08-3
Contact: Dawood B. Dudekula
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Sulte 4000, Baltimore, MD 21224-6820, USA
Email: cdna@lgsun.grc.nia.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 CTGGTGAAGCCTGGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGG 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.4%; Score 47; DB 6; Length 529;
100.0%; Pred. No. 2e-13;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="Hematopoietic Stem Cell
(Lin-/c-Kit-/Sca-1-)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="niaEST:K0716F08-5N"
/db_xref="taxon:10090"
/clone="NIA:K0716F08 IMAGE:30075139"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev stage="Age approx.10 weeks old"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                        (Lin-/c-Kit-/Sca-1-) cDNA Library (Long)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seg primer: M13 Reverse
High quality sequence stop: 529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 strain="C57BL/6NCr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                             Mus musculus (house mouse)
Mus musculus
             CA577954.1 GI:25126345
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: genome-reseggc.riken.jp, URL:http://genome.gsc.riken.jp/
Alzawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hirozand.F., Indicani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission Compute conputational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA
encyclopedia: real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Alzawa,K., Arakaya,T., Fukuda,M., Hara,A., Hasahizune,W., Imorani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Saki,K., Sasaki,D., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K0716F08-5N NIA Mouse Hematopoietic Stem Cell (Lin-/c-Kit-/Sca-1-)
CDNA Library (Long) Mus musculus cDNA clone NIA:K0716F08
IMAGE:30075139 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prepare mouse tissues.
Tissues ware provided by Vassilis Aidinis ( Biomedical Sciences
Research Center 'Al. Fleming' Institute of Immunology 14-16 Al.
Fleming street 16672 Vari, Greece ) whose assistance we gratefully
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Please visit our web site (http://genome.gsc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="whole joints"
/clone_lib="RIKEN full-length enriched, whole joints"
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100.0%; Pred. No. 1.9e-13;
iive 0; Mismatches 0;
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/db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                         Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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RESULT 12 CA577954

RESULT 13 BI104341

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  BI104341 558 bp mRNA linear EST 26-JUN-2001
602889919F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:5035013 5',
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Arakawa, T., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hiramoto, K., Hori, F., Ishii, Y., Ito, M., Kawai, J., Konno, H., Kouda, M., Koya, S., Matsuyama, T., Miyazaki, A., Nomura, K., Sano, H., Sasaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, Sano, H., Sasaki, T., Sasaki, T., Sagabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Shiraki, T., Tagami, M., Tagawa, A., Shiraki, F., Takeda, Y., Tanaka, T., Toya, T., Muramatsu, M. and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tisaue Procurement: Gilbert Smith, Ph.D.

Tisaue Procurement: Gilbert Smith, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:

http://image.llh.gov
Plate: LLAM11097 row: f column: 06

High quality sequence stop: 598.
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Stem cell origin."
/lab_host="DH10B"
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National Institutes of Health, Mammalian Gene Collection (MGC)
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    .598
    /organism="Mus musculus"

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/clone="IMAGE:5035013"
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                                                                                                     BI104341.1 GI:14555234
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                                                                                                                                                                                                                                                                                                                                 Unpublished (1999)
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                                                      mRNA sequence.
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AUTHORS
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was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3' end: BamHI." sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno, H., Pukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001)
Kondo, S., Shinaqawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
17-22 Suchiro-ch, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
Fax: 81-45-503-9216 /dev_stāgē="adult" /lab_host="DH108" /clone lib="RIKEN full-length enriched, adult male testis (DH108)" Email: genome-resaggsc.riken.jp, URL:http://genome.gsc.riken.jp/ Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected CDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. . 10 (10), 1617-1630 (2000) wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., and Hayashizaki,Y. Hayashizaki, Y.
Computational Analysis of Pull-Length Mouse cDNAs Compared with
Computational Sequences Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (http://genome.gsc.riken.go.jp/) for
further details. RIKEN integrated sequence analysis (RISA) system--384-format RIKEN Mouse ESTs (Arakawa,T., et al. 2001) Unpublished (2001) On Nov 4, 1999 this sequence version replaced gi:6246473. Contact: Yoshihide Hayashizaki organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="taxon:10090" 'tissue_type="testis" /clone="4930402P15"

Length 607; 6.4%; Score 47; DB 1; Let 100.0%; Pred. No. 2.1e-13;

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Livermore, CA, USA

Enaul: help@image.llnl.gov

This read has been verified (found to hit its original self in the correct orientation), as part of the I.M.A.G.E. Consortium quality control effort. High quality sequence is defined as having 100 or more base pairs with a phred quality value of 20 or greater, where a sliding window of 4 base pairs with a phred quality value of 15 or greater marks the beginning and end of the sequence. For information on obtaining this clone, please contact info@image.llnl.gov.

Plate: LiAMILOSY row: f column: 6
Seq primer: ml3rpl
High quality sequence stop: 640.
                                                                                                                                                                                                                         BQ109114 640 bp mRNA linear BST 16-APR-2002 imageqc_6_2001/snl21bdrr81.y1 NCI_CGAP_Lu29 Mus musculus cDNA clone INAGE:5035013 5', mRNA sequence.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 640)
Kale, P.I., Harsch, T.J., Folta, P.A., Nelson, D.O., Sanders, C.G. and Prange, C.K.
The I.M.A.G.E. Consortium quality control effort: clone resequencing for verification
Unpublished (2001)
Other_ESTS: BI104341
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/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH:
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/clone="IMAGE:5035013"
/tissue type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
          Gaps
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0
                                                                                       137 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGG 183
                                                  CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGG 77
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6.4%; Score 47; DB 5; Le
Best Local Similarity 100.0%; Pred. No. 2.1e-13;
Matches 47; Conservative 0; Mismatches 0;
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The I.M.A.G.E. Consortium
Lawrence Livermore National Laboratory
  0; Mismatches
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/organism="Mus musculus"
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BQ109114.1 GI:20158768
  47; Conservative
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122 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGG 168

Search completed: March 15, 2005, 23:20:20 Job time : 3434 secs

31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGG 77

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D13201 Mus musculu X02462 Mouse germl AC116524 Mus muscu AC073565 Mus muscu AX132007 Mus muscu U66461 Mus musculu AX436962 Mus musculu AX639151 Mus musculu AR276290 Mus muscul AR276290 Mus muscul AR276290 Mus muscul AR276290 Mus musculus AC079181 Mus musculus AC0791 Mus musculus AC079181 Mus musculus AC079181 Mus musculus AC0797 Mus musculus AC0797 Mus musculus AC089724 Mus musculu
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OXFORD BIOMEDICA LTD
OS Artificial Sequence
PN 40-2002
PP 04-300-2002
PF 04-300-1998 JP 1999501858
PF 04-300-1997 GB 9713150.2 PR PI SUSAN MARY KINGSMAN, CHRISTOPHER ROBERT BEBBINGTON, FIONA PI MILES WILLIAMD,
PI 
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1 (bases 1 to 729)
Kingsman, S.M., Bebbington, C.R., Ellard, F.M., Carroll, M.W. and
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/db_xref="taxon:32630"
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100.0%; Pred. No. 0;
:ive 0; Mismatches
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AC079181
AC090843
MUSIKCVRJ
AF162710
MMIGHT82
MUSAI
AF083186
MMIGGH9B
MMIGWH9
AC116524
AC073565
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AF303833
AY172007
AY436962
AY436
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AX002778 Sequence
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                                     GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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TNYMDLYGGQYTSYTVSSGGGGGGGGGGGGGGSSIVMTQTFPFLLVSAGDRYTITCKA
SQSYSENDYXMYQQKPGCSPFLLLSYTSSRYAGVPDRFIGSGYGTDFTFISTLQAEDL
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/note="unnamed protein product"
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   /mol_type="unassigned DNA"
/db_xref="taxon:32630"
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BEBRINGTON CHRISTOPHER ROBERT (GB); CARROLL MILES WILLIAM (GB);
ELLARD FIONA MARGARET (GB); KINGSMAN SUSAN MARY (GB); MYERS KEVIN
ALAN (GB); OXFORD BIOMEDICA LTD (GB)
TCTIGCAAGGCTTCTGGTTACTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC
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synthetic construct
other sequences artificial sequences.

E 1 (bases artificial sequences.

E 1 (bases artificial sequences.

Stratford, I.J., Patterson, A.V., Kingsman, S.M., Kan, O., Griffiths, L.
and Mitrophanous, K.

Enhancement of producy activation

Artificial Sequence

PN 47202505341-A/21

PP 19-FBB-2002

PP 05-MAR-1999 JP 2000534657

PR 06-MAR-1999 GB 9804841.6,19-AUG-1998 GB 9818103.5 PR
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N-1999 GB 9902081.0
IAN JAMES STRATFORD,ADAM VORN PATTERSON,SUSAN MARY KINGSMAN,ON
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A61K47/48,A61K35/76,A61K38/44,A61K45/00,A61K48/00,A61P9/10, PC
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Description of Artificial Sequence: Synthetic sequence FH
Location/Qualifiers
source
/organism='Artificial Sequence'.
Location/Qualifiers
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93.0%; Score 678; DB 6; Length 729;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 728; Conservative 0; Mismatches 1; Indels
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/organia="synthetic construct"
/mol type="genomic DNA"
/db_xref="taxon:32630"
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721 ATCAAACGG 729
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Bllard,F.M. and Myers,K.A.
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="5T4ScFv.1"
                        DNA
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                                                                                                                                                                                                                                                   Patent: WO 0136486-A 5 25-MAY-2001;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
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Sequence 5 from Patent WO0136486.
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Enhanced produce activation
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Fatent: WO 9945126-A 26 10-SEP-1999;
RINGSMAN SUBAN MARY (GB); MITROPHANOUS KYRIACOS (GB); PATTERSON
ADAM VORN (GB); STRAIFORD IAN JAMES (GB); GRIFFITHS LEIGH (GB); KAN
ON (GB); OXFORD BIOMEDICA LID (GB)
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 728; Conservative 0; Mismatches

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    /organism="synthetic const:
/mol_type="unassigned DNA"
    /db_xref="taxon:32630"

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/mol_type="unassigned DNA"
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SUSAN MARY KINGSMAN, CHRISTOPHER ROBERT BEBBINGTON, FIONA RILES WILLIAM CARROLL, KEVIN ALAN MYERS
C12N15/85, A61K48/00
Description of Artificial Sequence: cDNA Key
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                                                                                             /organism='Artificial Sequence'.
Location/Qualifiers
1. 1807
'organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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99.9%;
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                                             61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGGG
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                             TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC
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PN JP 2002507117-A/2
PD 05-MAR-2002
PP 04-JUN-1999 GB 9711579.4,20-JUN-1997 GB 04-JUL-1997 GB 9714230.1
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1 (bases 1 to 1807)
Kingsman, S.M., Bebbington, C.R., Ellard, F.M.,
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OXFORD BIOMEDICA LTD
OS Artificial Sequence
N JP 2002507117-A/2
PD 05-MAR-2002
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JP 2002507117-A/2.
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       CAGACTCCCACATTCCTGCTTGTTTCAGCAGGACAGGGTTACCATAACCTGCAAGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             other sequences; artificial sequences.
1 (bases 1 to 1467)
Kingsman, S.M., Bebbington, C.R., Ellard, F.M., Carroll, M.W. and
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    1467
    /organism='Artificial Sequence'.

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Description of Artificial Sequence: DNA
Key
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MILES WILLIAM CARROLL, KEVIN ALAN MYERS
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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04-JUN-1997 GB 9711579.
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OS Artificial Sequence
PN JP 2002507117-A/3
PD 05-MAR-2002
PF 04-UUN-1998 JP 199950
PR 04-UUN-1997 GB 971
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JP 2002507117-A/3.
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Best Local Similarity 99.9%;
Matches 725; Conservative (
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PI SUGAN WARY
MARGARET ELLARD,
PI MILES WILLI.
PC C12N15/85,A
CC Description
FH Key
FT SOURCE
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Patent: WO 9855607-A 2 10-DEC-1998;
Patent: WO 9855607-A 2 10-DEC-1998;
BEBBINGTON CHRISTOPHER ROBERT (GB); CARROLL MILES WILLIAM (GB);
ELLARD FIONA MARGARET (GB); KINGSWAN SUSAN MARY (GB); MYERS KEVIN
ALAN (GB); OXFORD BIOMEDICA LTD (GB)
Location/Qualifiers
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<3...1790
                      DNA
                                                                                                                                              other sequences; artificial sequences.
   AX002779 1807 bp
Sequence 2 from Patent WO9855607.
AX002779
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/protein_id="CAC04192.1" //db.xref="G1:1985108" //db.xref="G1:1985108" //tb.xref="G1:1985108" //tb.xref="G1:198510	Query Match 92.6%; Score 675; DB 6; Length 1467; Best Local Similarity 99.9%; Pred. No. 0; Matches 725; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Oy 1 GAGGTCCAGCTTCAGCAGTCTGGACCTGGACCTGGGGGCTTCAGTGAAGATA 60	Qy 61 TCCTGCAAGGCTTCTGGTTACTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120	Oy 121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACATGGTGTTACTCTCTAC 180	Qy 181 DACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240 Db 919 AACCAGAAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 978	Oy 241 ATGGAGGTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Oy 301 AIGAITACGAACTAIGITAIGGACTACTCGGGGTCAAGTAACCTCAGGCGTCACCGTCA 360	Qy 361 GGTGGTGGAGCGGTGGTGGTGGCGGCACTGGCGGCGGATCTAGTATTGTGATCACC 420	Oy 421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGACAGGGTTACCATAACCTGCAAGGCC 480 Db 1159 CAGACTCCCACATTCCTGCTTTCAGCAGGGACACAGGTTACCATAACCTGCAAGGCC 1218 Oy 481 AGTCAGAGTGTGAGTATGATGATGATGCAACCAACACAGAAGCCACACACA	Oy 541 CIGCICATAICCIAIACAICGCIACGCIAGGAICCCIGAICGCITCAITGGCAGT 600	QY 601 GGATATGGGACCGATTTCACTTTCACCATTACAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660 DD 1339 GGATATGGGACGGATTTCACTTTCACCATTACAGCACTTAGAGACCTGGAGATT 1398	Qy 661 TATTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAAGCACCAAGCTGGAA 720 Db 1399 TATTTCTGTCAGCAAGATTATAATTCTCCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1458	Oy 721 ATCAAA 726 	RESULT 11 AX149546 AX149546 1467 bp DNA linear PAT 08-JUN-2001
Qy 121 CATGGAAAGAGCCTTGAGTGACTTTAATCCTTAACATGGTGTTACTCTCTAC 180 Db 859 CATGGAAAGAGCCTTCAGTGAATTAATCCTTAACATGGTGTTACTCTCTAC 918 Qy 181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240 Db 919 AACCAGAAATTCAAGGACAAGAGCCATATTAACTGTAGACAAGTCATCCACACACGCTAC 240 C 241 ATGGAAGTCCCCCAACATCTGAAGACTCTGCGGTCTATTACTGTCCAACAGTCTACT 300 Cy 241 ATGGAAGTCCCCCAACATCTGAAGACTCTGCGGTCTATTACTGTCCAAGATCTACT 300 Db 979 ATGGAAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCCAAGATCTACT 300 Db 979 ATGGAAGCTCCGGACCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCCAAGATCTACT 1038	Qy 301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACGTCTCCTCA 360	Qy 361 GGTGGTGGCGGCGCTGGCGGCACTGGCGGATCTAGTATTGTGATGACC 420 1099 GGTGGTGGTGGCGGCGGCGGCGGCGGCGGGGGGGGGTCTAGTATTGTGATGACC 1158	OY 421 CAGACTCCCACATTCCTGCTTGTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 480	Qy 481 AGTCAGAGTGTGAGTATGATGTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540	Qy 541 CTGCTCATATCCTATACATCCAGTGGCTACGCTGGAGTCCCTGATCGCTTCGTTGGCAGT 600	Qy 601 GGATATGGGACTGACTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660 	Qy 661 TATTTCTGTCAGCAAGATTATAATTCTCCTCGACGTTCGGTGGAGGCACCAAGCTGGAA 720 	Qy 721 ATCAAA 726 	RESULT 10 AX002780 LOCUS LOCUS AX002780 AX002780 DEFINITION Sequence 3 from Patent W09855607. ACCESSION AX002780 AX002780 AX002780. AX002780.1 GI:9885107	ACTIONES SYNTHETIC CONSTRUCT ORGANISM SYNTHETIC CONSTRUCT OTHER Sequences; artificial sequences.	AUTHORS Bebbington, C.R., Carroll, M.W., Ellard, F.M., Kingsman, S.M. and Myers, K.A. TITLE Vector	Patent: BEBBING: ELLARD B	H	CDS 11467 /note="unnamed protein product" /codon_start=1 /transI_table=11

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PAT 18-SEP-2002
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                                                                                                                                                                                                                                   synthetic construct
synthetic construct
other sequences; artificial sequences.
(bases 1 to 1518)
Kingsman, S.M., Bebbington, C.R., Ellard, F.M., Carroll, M.W. and
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/organism='Artificial Sequence'
Location/Qualifiers
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OXFORD BIOMEDICA LTD

OX Artificial Sequence

PN JP 2002507117-A/5

PD 05-MAR-2002

PP 04-JUM-1997 GB 9711579.4,20-JUN-1997 GB

04-JUM-1997 GB 9711579.1,20-JUN-1997 GB

04-JUM-1997 GB 9714230.1

PI SUSAN MARY KINGSMAN, CHRISTOPHER ROBERT BEBBING

MARGARET ELLARD,

PI MALES WILLIAM CARROLL, KEVIN ALAN MYERS

PC C12N15/85,A61K48/00

CC Description of Artificial Sequence: DNA

FY SOURCE

//organism='Artificial Sequence: PNA

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//organism='Artificial Sequence
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Antibodies
Antibodies
Patent: WO 0136486-A 7 25-MAY-2001;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
1. 14677
/ organism="synthetic construct"
/ mol-type="unassigned DNA"
/ db xref="taxon:32630"
/ noTe="B7-1.5T48cFv.1"
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other sequences, artificial sequences.
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Sequence 7 from Patent WO0136486
AX149546
                                           AX149546.1 GI:14347985
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Patent: WO 0136486-A 11 25-MAY-2001;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
1. 1518
/organism="synthetic construct/mol_type="unassigned DNA"
/db xref="taxon:32630"
/note="B7-ScFv"
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Sequence 11 from Patent WO0136486.
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                                 1207 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC 1266
                                                                                                       1267 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1326
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BEBBINGTON CHRISTOPHER ROBERT (GB); CARROLL MILES WILLIAM (GB);
ELLARD FIONA MARGARET (GB); KINGSMAN SUSAN MARY (GB); MYERS KEVIN
ALAN (GB); OXFORD BIOMEDICA LTD (GB)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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                              AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGGCCTAC
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Bilard, F.M. and Myers, K.A.
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Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
1. 1796
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/noTe="5748cFV.1-IgG"
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TCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGC
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CAGCAGTCTGGACCTGACCTGGTGAAGCCTTGGGGGCTTCAGTGAAGATATCCTGCAAGGCT

75.6%; Score 551; DB 6; Length 1796; larity 99.6%; Pred. No. 4.3e-305; Conservative 0; Mismatches 3; Indels

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Aaq65623 HP1/2 lig Aaq659193 HP1/2 UV Aav66800 Anti-VLA-Aav66800 Anti-VLA-Aax15094 CDNA enco Aax27914 Anti-VLA-Aax86185 CDNA enco Aaf86185 CDNA enco Aaf86185 CDNA enco Ad125184 Murine HP Adf94348 Mouse ant Ad740361 Anti-VLA-Ad740361 Anti-VLA-Ad740361 Anti-VLA-Ad467072 Anti-GAE AAG9723 Anti-GAE AAG92207 Anti-Gisi Aag48038 Moncolona Aat66310 Single ch Ab822077 Anti-disi Aag48038 Moncolona Aag48038 Moncolona Aag48038 Moncolona Aag48038 Moncolona Aag48038 Moncolona Aag48038 Anti-Muma Aag38522 Hypercalc Ab515845 Anti-huma Ab515845 Anti-huma Ab515845 Anti-huma

Scoring table:

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Database :

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Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen; monoclonal antibody; single chain antibody; scFv; mouse; 5T4scFv.1; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New vector encoding a tumour interacting protein for treating cancer - contains a desired nucleotide sequence and/or protein which recognises tumours, and is used as a gene delivery system to treat cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This DNA sequence encodes a 5T4 scFv, designated 5T4scFv.1 (see AAW86002), comprising the heavy chain variable region (VH) from the murine 5T4 monoclonal antibody followed by a 15-amino acid flexible
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AAQ30754
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ADF94348
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97GB-00013150.
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Aaz19786 Anti-5T4
Aav80291 Anti-5T4
Aav80292 Human B7-
Aaf89730 Nucleotid
Aav80294 B7-16cFV
Aaf89732 Nucleotid
Aav80295 ScFV-1g51
Aav80295 ScFV-1g51
Aav80295 CCFV-1g51
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Aay3737 Anti-DNA
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         GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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linker and the light chain variable region (VL) of the mouse 5T4 antibody. The trophoblast cell surface antigen defined by monoclonal antibody 5T4 is expressed at high levels on the cells of a wide variety of human tumours. The 5T4scFv.1 DNA sequence can be used to construct single-chain antibodies (see AAV80291) and scFv fusion constructs (see sequence coding for a tumour interacting protein (TIP) and optionally a nucleotide sequence of interest (NOI) which encodes a protein of interest (MOI) the vector being capable of delivering the NOI and/or POI to the tumour recognised by the TIP. Delivery can be in vivo or ex vivo. The vector is used to treat cancer, and may also used as a gene delivery expert its used to treat cancer, and may also used as a gene delivery expert its used to treat cancer, and may also used as a gene delivery experts.
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100.0%; Pred. No. 0;
ive 0; Mismatches
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Best Local Similarity
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The specification describes the use of a single chain antibody (ScFv), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The ScFv antibody is useful in the manufacture of a medicament, for affecting a disease in vivo, for preparing a pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The ScFv antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune diseases, cancers, central nervous system disorders including Parkinson's disease, periodontal diseases, cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-related diseases, and other immune disorders. The present sequence encodes a 5T4 ScFv of the invention. The antibody comprises the VH and VL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from murine 574 monoclonal antibody, joined by a linker sequence
                                                                                                                                                                      hypersensitivity; autoimmune disease; central nervous system disorder; Parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.
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                                                                                                                                                      Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
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                                                                                                                    Nucleotide sequence of a 5T4 ScFv designated 5T4ScFv.1.
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100.0%; Pred. No. 0;
ive 0; Mismatches 0;
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2000GB-00005071.
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                AAF89729 standard; DNA; 729
                                                                                  (first entry)
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les 729; Conservative
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                                                  AAF89729;
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ATCAAACGG 729

601 661 661 721

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This sequence represents an example of a DNA encoding a secreted single chain antibody FV fragment, which is involved in transcellular chain antibody FV fragment can be fused to cocalisation. In this example, the antibody FV fragment can be fused to antigen. A secreted single chain antibody FV fragment can be fused to cytochrome P450 reductase (P450R) derivatives such as anchorless P450R (AAV4228F) or FV fragment (AAV4228B). This enables the fusion protein to be delivered to other cells where it is then transported to the nucleus. Many drugs' sites of action are in the nucleus, rather than the cytoplasm, where P450R normally functions. P450R or its derivatives can be used to activate prodrugs to their active form via reduction. Administration of a prodrug is useful where the active drug may be metabolised before it reaches its site of action or where the active drug is cytotoxic, e.g., anticancer drugs. Targetted delivery of such prodrug is cytotoxic, e.g., anticancer drugs. Targetted delivery of such prodrug cativators allows a reduction in dose of the prodrug, and thus of activators allows a reduction in dose of the prodrug, and thus of express them, are specifically used to treat tumours, inflammation, catherosclerosis and muscular dystrophy, but may also be used to treat many other conditions associated with hypoxia, isochaemia or hypoglycemia, or to conditions associated with hypoxia, isochaemia or hypoglycemia, or to deliver antibiotics, antivial agents analdeagosic, ansesthetics, anti-
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                                                                                                                                                                                                                                                            New prodrug activating agent targeted to selected cells or tissues, particularly hypoxic cells, for treating e.g. tumors.
                                                                                                                                                              Griffiths L;
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                                                                                                                                                              Patterson AV, Kingsman SM, Kan O,
                                                                                                                                                                                                                                                                                                               Example 9; Fig 3; 187pp; English
                                                                                                                              (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                            98GB-00018103.
99GB-00002081.
                                99WO-GB000674
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Matches 728, Conservative
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P-PSDB; AAY42294.
                                                                                                                                                            Stratford IJ, 1
Mitrophanous K;
                                                                              19-AUG-1998;
29-JAN-1999;
                                05-MAR-1999;
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                                                                                 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTTAC
                                                                                                                                               ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACGTCTCCTCA
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                                TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC
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/trag= a
/roduct= "Anti-5T4 secreted single chain antibody Fv
fragment"
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The invention provides a new prodrug activating agent that comprises: (i) a localization domain (LD; other than a tumor-selective antibody) and a prodrug activating domain (BD); (ii) at least one nucleic acid encoding a cytochrome P450 and under control of at least one constitutive or inducible expression control sequence or (iii) a modified hematopoietic stem cell (MHSC) containing at least one nucleic acid encoding a PAD and cunder control of elements as in (ii). The prodrug activating agent or under control of elements as in (ii). The prodrug activating agent or vectors that express them, are specifically used to treat tumors.

CC inflammation, atherosolarosis and muscular dystrophy, but may also be used to treat many other conditions, e.g. crebral malaria, rheumatoid arthritis, or conditions associated with hypoxia, hypoglycemia or strhing, or conditions associated with hypoxia, hypoglycemia or constitution and dispussing catherics, anti-inflammatories, antineoplastic agents and diagnostic agents. LD optimize activity of PAD, e.g. by delivering it to selected cannesthetics, nucleic acids encoding the agent may be expressed selectively in phypoxic cells. The present sequence represents the DNA encoding the single chain variable antibody fragment against the tumor antigen ST4 scPv). ST4 scPv is used in the construction of a fusion protein comprising ST4 scPv and a human P450 reductase derivative alP450R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prodrug; localization domain; tumor-selective antibody; cytochrome P450; prodrug activating domain; modified hematopoietic stem cell; MHSC; tumor; inflammation; atherosclerosis; muscular dystrophy; cerebral malaria; rheumatoid arthritis; hypoxia; ischemia; hypoglycemia; tumor antigen;
                                                                            CAGACTCCCACATTCCTGCTTTCAGCAGGAGACAGGCTTACCATAACCTGCAAGGCC
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98GB-00018103.
99GB-00002081.
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19-AUG-1998;
29-JAN-1999;
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AAZ07810 RESULT

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601 601

New prodrug activating agent targeted to selected cells or tissues, particularly hypoxic cells, for treating e.g. tumors or inflammation.

WPI; 1999-540852/45.

Mitrophanous K;

P-PSDB; AAY27407.

Example 9; Fig 3F; 149pp; English.

099

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This DNA sequence encodes a single chain antibody (Sab), termed 574Sabl (see AAW86003), comprising an scrv derived from murine monoclonal antibody 574 (see AAW86002) and the human gl constant region. It was constructed from cassettes comprising a translation initiation signal and signal peptide (see AAV80297), the sequence of the secreted portion of 574scrv.1, and the sequence of the human gl constant region genomic clone. The trophoblast cell surface antigen defined by 574 is expressed at high levels on the cells of a wide variety of human tumours. The invention relates to a vector comprising a nucleotide sequence coding for a tumour interacting protein (TIP) and optionally a nucleotide sequence of interest (NOI) which encodes a protein of interest (EDI), the vector being capable of delivering the NOI and/or POI to the tumour recognised by the TIP. Delivery can be in vivo or ex vivo. The vector is used to treat cancer, and may also used as a gene delivery system for introducing at least I gene encoding a TIP (preferably a tumour binding protein) into a haematopoietic cell lineage
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                                    TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA
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TATTICIGICAGCAAGATTATAATICICCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA
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97GB-00013150.
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Homo sapiens.
Synthetic.
Chimeric.
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20-JUN-1997;
04-JUL-1997;
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Sequence 1807 BP; 432 A; 543 C; 469 G; 363 T; 0 U; 0 Other;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen; monoclonal antibody; gingle chain antibody; scFv; mouse; human; B7-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 caccircaccricaccacricacaccricaccricaaccricaccricaccricaccricacracara
                                                                                                                                                                             249 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGGCCTAC
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                                                                                                                                  129 recrecaaegerreregrraerearreacreceraeraeareaegegegegegegege
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                                                                                                                                                                                                                                                                        241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGGTCTATTACTGTGCAAGATCTACT
                                                                                                                                                                                                                                                                                                                             ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA
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 Length 1807;
                                                      1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCT
                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human B7-1.5T4.1 gene fusion, specific for human 5T4.
 DB 2;
93.0%; Score 678; DE
larity 99.9%; Pred. No. 0;
Conservative 0; Mismatches
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Query Match
Best Local Similarity
Matches 728; Conserv
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Homo sapiens.
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1099 GGTGGTGGTGGTGGTGGTGGTGGCCACTGGCGGCGGCGGTGTTTGTGTTGTGATGACC 1158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single chain antibody, ScFv; inflammatory disease, arthritis, cancer; hypersensitivity, autoimmune disease; central nervous system disorder; Parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.
    GGTGGTGGTGGTGGTGGTGGCGCCACTGGCGGCGCGCGGATCTAGTATTGTGATGACC
                                                                                                                                                                                                                   AGTCAGAGTGTGAGTAATGATGATGTAGCTTGGTACCAACAGAAGCCAGGCAGTCTCCTACA
                                                                                               CAGACTCCCACATTCCTGCTTGTTTCAGCAGGACAGGGTTACCATAACCTGCAAGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleotide sequence of a B7-1.5T4.1 fusion protein.
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1. .1467
/*tag= a
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2000GB-00003527.
2000GB-00005071.
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Homo sapiens.
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15-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This DNA sequence encodes B7-1.5T4.1 (see AAW86004), a fusion protein comprising the extracellular domain (amino acids 1-215) of human cost stimulatory molecule B7-1 joined via a flexible peptide linker to an scrv (see AAW86002) derived from murine 5T4 monoclonal antibody. The cDNA can be inserted into vector pCI to allow expression of the fusion protein in mammalian cells. The trophoblast cell surface antigen defined by 5T4 is expressed at high levels on the cells of a wide variety of human tumours. The invention relates to a vector comprising a nucleotide sequence coding for a tumour interest (NOI) which encodes a protein of interest (POI), the sequence of interest (NOI) which encodes a protein of interest (POI), the vector being capable of delivering the NOI and/or POI to the tumour corrector being capable of delivering the NOI and/or POI to the tumour corrector cancer, and may also used as a gene delivery system for introducing at least 1 gene encoding a TIP (preferably a tumour binding protein) into a haematopoietic cell lineage. B7-1 is expected to bind specifically to CD28 and CTLA-4 present on human T-cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACGTCTCCTCA 1098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      New vector encoding a tumour interacting protein for treating cancer - contains a desired nucleotide sequence and/or protein which recognises tumours, and is used as a gene delivery system to treat cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GAGGICCAGCITCAGCAGICIGGACCIGACCIGGIGAAGCCIGGGGCTICAGIGAAGAIA
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Pred. No. 0;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1467 BP; 394 A; 349 C; 352 G; 372 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                             Carroll MW,
                                                                                                                                                                                                                                                                                                                                           Bebbington CR, Ellard FM,
                                                                                                                                                                                                                                                                                             (OXFO-) OXFORD BIOMEDICA UK LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 5; Fig 2; 82pp; English.
                                                                                                                                                                                                97GB-00011579.
97GB-00013150.
97GB-00014230.
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P-PSDB; AAW86004.
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                                                                                                                                                                                                                                                                                                                                           Kingsman SM,
                                                                W09855607-A2
                                                                                                                                                          04-JUN-1998;
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                                                                                                             10-DEC-1998
Synthetic.
Chimeric.
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15-MAR-1999
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                                                                                                                                          The specification describes the use of a single chain antibody (ScFv), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The ScFv antibody is useful in the manufacture of a medicament, for affecting a disease in vivo, for preparing a pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The ScFv antibody is also useful for treating inflammatory disease. The ScFv antibody is also useful for treating inflammatory disease, including arthritis, hypersensitivity, autoimmune disease, cancers, central nervous system disorders including Parkinson's disease, periodontal diseases, cardiopulmonary diseases, cardiovascular diseases, and other immune disorders. The present sequence encodes a B7-1.5T4.1 fusion protein. This comprises the N-terminus of the 5T4 SCFv is fused after amino acid 215 of human B7-1
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This DNA sequence encodes a fusion protein comprising the extracellular domain of mouse co-stimulatory molecule B7-1 joined via a flexible peptide linker to an acry (see AAW86002) derived from murine 574 monoclonal antibody. The fusion can be used to construct a recombinant vector, e.g. retrovirus, lentivirus, adenovirus, poxvirus, vaccinia virus corbaculovirus, used for direct treatment of tumour patients. The trophoblast cell surface antigen defined by 574 is expressed at high levels on the cells of a wide variety of human tumours. The invention relates to a vector comprising a nucleotide sequence coding for a tumour interacting protein (ITP) and optionally a nucleotide sequence of interacting protein (ITP) and optionally a nucleotide sequence of interest (NOI) which encodes a protein of interest (POI), the vector being capable of delivering the NOI and/or POI to the tumour recognised by the TIP. Delivery can be in vivo or ex vivo. The vector is used to treat cancer, and may also used as a gene delivery system for introducing a least 1 gene encoding a TIP (preferably a tumour binding protein) into a haematopoietic cell lineage. B7-1 binds specifically to CD28 and CTLA-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen; monoclonal antibody; gingle chain antibody; scFv; mouse; B7-1;
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Pred. No. 9.6e-270;
0; Mismatches 3; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bebbington CR, Ellard FM, Carroll MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                B7-1/scFv specific for use in cancer gene therapy.
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                                                                                                                                                                                         BP.
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                                                                                                                                                                                         AAV80294 standard; cDNA; 1518
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(first entry)
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1459 ATCAAA 1464
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Ellard FM;

Carroll MW,

Kingsman SM, Bebbington CR,

(OXFO-) OXFORD BIOMEDICA UK LTD

99WO-GB003859. 2000GB-00003527. 2000GB-00005071.

13-NOV-2000; 2000WO-GB004317.

8; Fig 5; 118pp; English.

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The specification describes the use of a single chain antibody (ScFv), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The ScFv antibody is useful in the manufacture of a medicament, for affecting a disease in vivo, for preparing a pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The ScFv antibody is also useful for treating inflammatory diseases. The ScFv antibody is also useful for treating diseases, cancers, central nervous system discases including arthritis, hypersensitivity, autoimmune disease, periodontal diseases, cardiopulmonary diseases, cardiovascular diseases, pastrointestinal diseases, infections, diabetes, Helicobacterrelated diseases, and other immune disorders. The present sequence encodes a B7 link ScFv sequence. A human B7 sequence is linked to a ScFv of the invention
                                                                                                                                                                                              Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
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                                                                                                                                                                   WPI; 2001-343805/36.
                                           15-FEB-2000;
02-MAR-2000;
                           18-NOV-1999;
                                                                                                                      Kingsman A,
                                                                                                                                    Myers KA;
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Length 1518;
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79.0%; Score 576; DB 4; 1 99.6%; Pred. No. 9.6e-270;
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Single chain antibody; ScFv; inflammatory disease; arthritis; cancer; hypersenaitivity; autoimmune disease; central nervous system disorder; Parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.

WO200136486-A2 Synthetic. Homo sapiens.

25-MAY-2001

Nucleotide sequence of a B7 link ScFv sequence.

(first entry)

23-JUL-2001

AAF89732;

BP

AAF89732 standard; DNA; 1518

480

540

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Gaps

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140 132 200 192 260 252 320 312 380 372 440 432 500 492 560 552 620 612 680 672 740

72

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pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The ScFv antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune diseases, cancers, central nervous system disorders including Parkinson's disease, periodontal diseases, cardiopulmonary diseases, cardiovascular diseases, inflatinal disorders, infections, diabetes, Helicobacterrelated diseases, and other immune disorders. The present sequence encodes an Ig-574 fusion protein
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                                                                                                                                                                                 Length 1796;
                                                                                                                                                 Sequence 1796 BP; 429 A; 539 C; 466 G; 362 T; 0 U; 0 Other;
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                                                                                                                                                                            Score 551; DB 4;
Pred. No. 1.4e-257;
0; Mismatches 3;
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                                                                                                                                                 1446
                                                                                                                                                                                                               TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The specification describes the use of a single chain antibody (ScFv), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The ScFv antibody is useful in the manufacture of a medicament, for affecting a disease in vivo, for preparing a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single chain antibody, ScFv; inflammatory disease, arthritis, cancer, hypersensitivity, autoimmune disease, central nervous system disorder; Parkinson's disease, periodontal disease, cardiopulmonary disease; cardiovacular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.
                     AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA
                                                                         CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT
                                                                                                                                               GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT
                                                   CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT
                                                                                                                 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT
                                                                                                                                                                                 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
12. :1790
/*tag= a /transl_except= (1518. :1520, aa: Met)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleotide sequence of an Ig-5T4 fusion protein.
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15-FEB-2000; 2000GB-00003527.
02-MAR-2000; 2000GB-00005071.
                                                                                                                                                                                                                                                                                                                                                             DNA; 1796
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                                                                                                                                                                                                                                                                    ATCAAACGG 1515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-343805/36.
                                                                                                                                                                                                                                               ATCAAACGG
                                                                                                                                                                                                                                                                                                                                                             standard;
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Mus sp.
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GTCAGAGTGTG

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381 TATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACGTCTTCTTCAGGTGGTGGTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-343805/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200136486-A2.
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02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kingsman A,
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                                                 441
                                                                         433
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                                                                                                                                                                                                                                                                                                                                                                               This DNA sequence encodes a fusion protein comprising the human IgEl heavy constant region joined via a flexible peptide linker to an scPv (see AAW86002) derived from murine 574 monoclonal antibody. The fusion construct can be incorporated into a recombinant viral vector for use in gene therapy of cancer. The trophoblast cell surface antigen defined by 574 is expressed at high levels on the cells of a wide variety of human tumours. Binding of IgE to tumour cells should promote a strong histamine and hence inflammatory response and destruction of tumour cells. The invention relates to a vector comprising a nucleotide sequence coding for a tumour interacting protein (ITP) and optionally a nucleotide sequence of interest (NOI) which encodes a protein of interest (POI), the vector being capable of delivering the NOI and/or POI to the tumour recognised by the TIP. Delivery can be in vivo or ex vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCCATGGAAAGAGC 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTGGTTACTCATTCACTGGCTACTACATGCACTGGAAGCAGAGCCATGGAAAGAGC 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITGAGIGGAITGGACGIAITAAICCTAACAAIGGIGITACTCICIAAAACCAGAAAITC 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTTCTACAACCAGAAATTC 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGGCTACATGGAGCTCCGC 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACACGCCTACATGGAGCTCCGC 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCCTGACATCTGAGGACTCTGTGTGTTTACTGTGCAAGATCTACTATGATTACGAAC 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACGTCTCTCAGGTGGTGGTGGTGG
         Tumour interacting protein; cancer; gene therapy; vector; 574 antigen; monoclonal antibody; single chain antibody; scFv; mouse; human; IgE1; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72
                                                                                                                                                                                                                                                                                                        New vector encoding a tumour interacting protein for treating cancer - contains a desired nucleotide sequence and/or protein which recognises tumours, and is used as a gene delivery system to treat cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGCAGTCTGGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCT
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Pred. No. 1.4e-257;
0; Mismatches 3; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2090 BP; 461 A; 653 C; 565 G; 411 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                           Carroll MW,
                                                                                                                                                                                                                                                          Bebbington CR, Ellard FM,
                                                                                                                                                                                                                                                                                                                                                           Example 13; Page 64; 82pp; English
                                                                                                                                                                                                                                   BIOMEDICA UK LTD
                                                                                                                                                                                                          97GB-00014230.
                                                                                                                                                            98WO-GB001627
                                                                                                                                                                                  97GB-00011579
                                                                                                                                                                                                97GB-00013150,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.6%;
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                                                                                                                                                                                                                                                                                 WPI; 1999-059910/05.
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                                                                                                                                                                                                                                 (OXFO-) OXFORD
                                                        Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                          Kingsman SM,
                                                                                                         WO9855607-A2
                                                                                                                                                          04-JUN-1998;
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                                                                                  Chimeric.
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                                                                                                                                                                                                                      552
                                                                                                                                                                                                                                                                                     620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          681 GATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTTATTTCTGTCAG 740
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypersensitivity, autoimmune disease, central nervous system disorder; Parkinson's disease, periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.
                                                                                                                  501 TTCCTGCTTGTTTCAGCAGGAGAACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTG
AGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACCCCAGACTCCCACA
                                                                      TTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGTG
                                                                                                                                                                                                                                                                          AGTAATGATGTAGCTTGGTACCAAAGCCAGGGCAGTCTCCTACACTGCTCATATCC
                                                                                                                                                                                                                                                                                                                                                                                                            621 TATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTGGATATGGGACG
                                                                                                                                                                                                                      AGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGCAGTCTCCTACACTGCTCATATCC
                                                                                                                                                                                                                                                                                                                                                            TATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTGGATATGGGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ä,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of a SvFv-1gE protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 11; Fig 7; 118pp; English
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2000GB-00005071.
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88.

Sugamura K;

Kanayama Y,

Nakazawa H,

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MAb capable of binding to the gamma chain of the IL-2 receptor, and thus of blocking the IL-2 response, is produced by mouse hybridoma line GP-4 (FRRM BP-4640). DNA encoding the variable region of this MAb was expressed in B. coli, yielding FV(GP-4) with immumosuppressive activity. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31 CTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   397 CTGGTGAAGCCTGGGGGCTTCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTACTCATTCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunosuppressant polypeptide - has ability to block interleukin-2
                                                         MAb; monoclonal antibody; hybridoma; interleukin-2; IL-2; Fv; antibody variable region; GP-4; Fv(GP-4); immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 11.8%; Score 86; DB 2; Length 729; Best Local Similarity 100.0%; Pred. No. 2.3e-31; Matches 86; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 729 BP; 199 A; 169 C; 182 G; 179 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 GGCTACTACATGCACTGGGTGAAGCA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 18; Page 29; 37pp; English
                                                                                                                                                                                                                                                                                       94EP-00106257.
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                                                                                                                                                                                                                                                                                                                                                              94JP-00036065
       Fv(GP-4) immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hamura J,
                                                                                                                                                                                                                                                                                                                                                                                                                (AJIN ) AJINOMOTO KK
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Homo sapiens.
Chimeric.
                                                                                                                                                                                                                                                                                       21-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                              07-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shimamura T,
Takeshita T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUN-2004
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                                                                                                                                      Мив вр.
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ADM72026
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pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The ScFv antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmund diseases, cancers, central nervous system disorders including Parkinson's disease, periodontal diseases, cardiopulmonary diseases, cardiovascular diseases, astrontestinal disorders, infections, diabetes, Helicobacterrelated diseases, and other immune disorders. The present sequence encodes a ScFv of the invention linked to an IgE sequence
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                                                                                                                                                                                                                                                                            Score 551; DB 4; Length 2090;
Pred. No. 1.4e-257;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                     Sequence 2090 BP; 461 A; 654 C; 564 G; 411 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.6%;
Matches ,701; Conservative
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(first entry)
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09-MAY-1995
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Gaps

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GPC3; glypican 3; anti-GPC3 antibody; cell disruption; anti-cancer; cytostatic; gene; ds; MIE07.
                                                                                                              Chimeric mouse-human antibody MIE07 heavy chain encoding DNA
                                                                                                                                                                                                                   /*tag= a
/product= "M1E07 heavy chain"
457 GGCTACTACATGCACTGGGTGAAGCA 482
                                                                                                                                                                                                Location/Qualifiers
                                                       BP
                                                      ADM72026 standard; DNA; 1413
                                                                                           (first entry)
                                                                                                                                                                                                           .1413
                                                                                                                                                                                                                                                WO2004022739-A1
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Anti-DNA antibody which specifically binds DNA hairpin - useful develop prods. for diagnosis and treatment of disorders, e.g. glomerulonephritis or systemic lupus erythematosus.

WPI; 1997-011854/01.

Example; Fig 7; 102pp; English

Tokita S;

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The invention relates to an antibody against the N terminus of glypican 3 (GPC3). The antiboduy can be used for causing cell disruption and can be uses as an anti-cancer agent. The present sequence represents a chimeric mouse-human antibody MIE07 heavy chain encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                               31 CTGGTGAAGCCTGGGGCCTTCAGTGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACT 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heavy chain; variable region; anti-DNA; monoclonal; antibody; MAb 7b3; hairpin; diagnosis; inflammatory glomerulonephritis; systemic lupus erythematosus; screening; treatment; prevention; SLB;
                                                                                                                                                                                 Antibody against the N terminus of glypican 3(GPC3) causes cell disruption and is useful as an anticancer agent.
                                                                                                                                                                                                                                                                                                                                          Query Match
11.8%; Score 86; DB 12; Length 1413;
Best Local Similarity 100.0%; Pred. No. 2.2e-31;
Matches 86; Conservative 0; Mismatches 0; Indels (
                                                                                                                  Aburatani H, Midorikawa Y, Nakano K, Ohizumi I, Ito Y,
                                                                                                                                                                                                                                                                                                                Sequence 1413 BP; 340 A; 436 C; 372 G; 265 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-DNA antibody 7b3 heavy chain variable region cDNA.
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/note= "no STOP codon given"
                                                                                                                                                                                                                        Example 4; SEQ ID NO 11; 122pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                91 GGCTACTACATGCACTGGGTGAAGCA 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 GGCTACTACATGCACTGGGTGAAGCA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                      04-SEP-2003; 2003WO-JP011318,
                                                               04-SEP-2002; 2002WO-JP008999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
(first entry)
                                                                                         (CHUS ) CHUGAI SEIYAKU KK
                                                                                                                                             WPI; 2004-269573/25.
                                                                                                                                                          P-PSDB; ADM72027
             18-MAR-2004
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12-AUG-1997
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95US-00443540. 96WO-US007113

16-MAY-1996; 18-MAY-1995;

WO9636361-A1

21-NOV-1996.

Glick GD, Swanson PC; (UNMI) UNIV MICHIGAN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 334 BP; 93 A; 79 C; 83 G; 79 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 9.1%; Score 66; DB 2; Le Similarity 100.0%; Pred. No. 1.3e-21; 6; Conservative 0; Mismatches 0;
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The present sequence encodes the heavy chain variable region of the anti-DNA monoclonal antibody (MAb) 7b3, which has a high affinity for single stranded DNA, how or no affinity for double stranded DNA and specifically binds a DNA hairpin. The MAb can be used diagnose disorders associated with the pathological complexation of DNA, e.g. inflammatory a Johnerullonephritis and systemic lupus erythematosus. It can also be used to generate reagents to soreen for pharmaceutical agents, and treat and/or prevent an above disorder. Calf thymus DNA was used to immunise a MRL-lpr mouse, spleen cells from which were then fused with Sp2/0 myeloma cells to give hybridomas producing the anti-DNA MAb. 7b3 was found to react strongly with poly(dT), poly(dG) and poly(dI), moderately with single stranded DNA and weakly with poly(G). (Updated on 27-AUG-2003 to

correct OS field.)

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US-08-230-843-3
RESULT 1
Sequence 3, Appli
Sequence 11, Appli
Sequence 24, Appli
Sequence 24, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 2, Appli
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Appli
Appli
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                                                    March 15, 2005, 20:44:30 ; Search time 236 Seconds (without alignments) 5054.431 Million cell updates/sec
                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 26,
Sequence 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 49,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 49,
Sequence 49,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6,
Sequence 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1,
                                                                                                                                                                                                                                                                                                                                                  Description
                                                                                                   1 gaggtccagcttcagcagtc......ccaagctggaaatcaaacgg
                                                                                                                                                                        2405568
                                                                                                                                                                                                                            Issued Patents NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                               US-08-398-612A-49
US-08-398-611A-49
US-08-396-851A-49
                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                         1202784 segs, 818138359 residues
                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                              Post-processing: Listing first 45 summaries
                                     - nucleic search, using sw model
                                                                                                                  OLIGO_NUC
Gapop_60.0 , Gapext 60.0
                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                   US-10-016-686-5
729
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                              906
318
318
318
318
318
318
718
714
405
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405
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                                                                                          Perfect score:
Sequence:
                                                                                                                  Scoring table:
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                                     OM nucleic
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                                                                                                                                                                                                                              Score 86; DB 2; Length 729;
Pred. No. 1e-33;
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100.0%; Pred. No. 10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Konski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFRENCE/DOCKET NUMBER: 2034
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (650) 494-0792
TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
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Best Local Similarity 100.
Matches 66; Conservative
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Best Local Similarity
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          ; NAME/KEY:
; LOCATION:
US-08-636-936-3
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STATE: C2
COUNTRY:
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GENERAL INFORMATION:
APPLICANT: SHIMAMURA, TOSHIRO
APPLICANT: HAWIRO, JUNJI
APPLICANT: NAKAZAWA, HARUMI
APPLICANT: KANAYAWA, YUKA
APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKESHITA, TOSHIKAZU
ITILE OF INVENTION: IMMUNOSUPPRESSANT
NUMBER OF SEQUENCES: 12
CORRESSEDINDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
                                                                                                                                                                                                                                                                                                          Query Match
11.8%; Score 86; DB 1; Length 729;
Best Local Similarity 100.0%; Pred. No. 1e-33;
Matches 86; Conservative 0; Mismatches 0; Indels
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1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/636,936
FILING DATE: 24-APR-1996
CLASSIFICATION: 424
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APPLICATION D47:
APPLICATION NUMBER: US 08/230,843
FILING DATE: 21-APR-1994
APPLICATION NUMBER: UP 094491/1993
FILING DATE: 21-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UP 036065/1994
FILING DATE: 07-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, NO. 5885140man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 24,618
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91 GGCTACTACATGCACTGGGTGAAGCA 116
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MOLECULE TYPE: Other nucleic acid
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Patent No. 5856140
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TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 729 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
                                                                                            ), NAME/KEY:
; LOCATION:
US-08-230-843-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 2
US-08-636-936-3
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8 CIGGIGAAGCCTGGGGGCTTCAGIGAAGATATCCTGCAAGGCTTCTGGTTACTCATTCACT 67
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                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0,
APPLICATION NUMBER: US/08/881,037
FILING DATE: 23-UM-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/443,540
FILING DATE: 18-MAY-1995
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.1%; Score 66; DB 3; L
100.0%; Pred. No. 1.6e-23;
Live 0; Mismatches 0;
Sequence 11, Application US/08881037
Fatent No. 6080588
GENERAL TIPORMATION:
APPLICANT: Swanson, Patrick C.
TILLE OF INVENTION: DNA BINDING ANTIBODIES
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSE: MORTIBOD & Poerster
STREET: 755 Page Mill Road
CITY: Palo Alto
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APPLICANT: Davis, Pamela B.
APPLICANT: Davis, Pamela B.
TITLE OF INVENTION: Serpin Enzyme Complex Receptor TITLE OF INVENTION: Mediated Gene Transfer NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS: ADDRESSE: Medlen & Carroll STREET: 220 Montcome...
                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/217,847
                                                                                                                        Medlen & Carroll
JIREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTEY: United State? CIP: 94104
COMPUTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO WO 95/25809
FILING DATE: 23-MAR.1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/216,534
FILING DATE: 23-MAR.1994
ATTORNEY/AGRAT INFORMATION:
                                                                                                                                                                                                                                                                                                ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Patent No. 6200801
GENERAL INFORMATION:
APPLICANT: Ferkol Jr., Thomas W. APPLICANT: Davis, pamela B. APPLICANT: Ziady, Assem-Galal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/656,906
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027 REFERENCE/DOCKET NUMBER: CAL TELECOMMUNICATION INFORMATION: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 24
SEQUENCE CHARACTERISTICS:
LENGTH: 906 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 100.
Matches 63; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION:
US-09-217-847-24
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                                                                            Sequence 24, Application US/08656906
Patent No. 2972901
GENERAL INFORMATION:
APPLICANT: Ferkol Jr., Thomas W.
APPLICANT: Davis, Pamela B.
APPLICANT: Ziady, Assem-Galal
TITLE OF INVENTION: Serpin Enzyme Complex Receptor
TITLE OF INVENTION: Mediated Gene Transfer
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PAPLICATION NUMBER: US/08/656,906
FILING DATE: 03-JUN-1996
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                  ADDRESSEE: Medlen & Carroll
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
COUNTRY: United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Prec. ...
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APPLICATION NUMBER: US 08/
TILING DATE: 03-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO WO 95/25809
FRIOR APPLICATION NUMBER: WO WO 95/25809
PRIOR APPLICATION NUMBER: US 08/216,534
PRIOR APPLICATION DATA: 23-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: CASE-02280
TELECOMMUNICATION: NUMBER: CASE-02280
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 906 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100. Matches 63; Conservative
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LOCATION: 1..9
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                                                                      JS-08-656-906-24
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RESULT 5 US-09-217-847-24 ; Sequence 24, Application US/09217847

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385 CAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGC 444
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8.6%; Score 63; DB 3; Length 906;
100.0%; Pred. No. 5.6e-22;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Papayannopoulou, Thalia (USA only)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Board of Regents, U.
Washington (except USA)
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08463128
Patent No. 5695755
GENERAL INFORMATION:
APPLICANT: Papayamopoulou, Thal
APPLICANT: Washington (except US
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linear
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Patent No. 5824304
GENERAL INFORMATION:
APPLICANT: Papayannopoulou, Thalia (USA only)
APPLICANT: Board of Regents, U.
APPLICANT: Washington (except USA)
TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC STEM
TITLE OF INVENTION: CELLS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
  PERIPHERALIZATION OF HEMATOPOIETIC STEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 8.5%; Score 62; DB 1; Length 318; Best Local Similarity 100.0%; Pred. No. 1.8e-21; Matches 62; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                          SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,128
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER: US 07/977,702
FILING DATE: 11-11-1993
APPLICATION NUMBER: US 07/977,702
FILING DATE: 11-3-NOV-1992
ATTORNEY AGENT INFORMATION:
NAME: Haley Jr., James F.
REFERENCE/POCKET NUMBER: B173CIP
TELECOMMUNICATION NUMBER: B173CIP
                                                                             SEE: C/O FISH & NEAVE
: 1251 Avenue of the Americas
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: c/o FISH & NEAVE
1251 Avenue of the Americas
                                                                                                                                                   STATE: New York
COUNTRY: U.S.A.
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE PORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 318 base pairs
TYPE: nucleic acid
TITLE OF INVENTION: PEI
TITLE OF INVENTION: CEI
NUMBER OF SEQUENCES: 1(
CORRESPONDENCE ADDRESS:
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STATE: New York
COUNTRY: U.S.A.
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                                                                                      ADDRESSEE:
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432 ATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 491
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TITLE OF INVENTION: PERIPHERALIZATION OF HEMATOPOIETIC STEM
TITLE OF INVENTION: CELLS
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: c/o FISH & NEAVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 62; DB 1; Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
PILITATION NUMBER: US/08/436,339A
FILING DATE:
         PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1.8e-21;
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Patent No. 5843438
GENERAL INFORMATION:
APPLICANT: Papayannopoulou, Thalia (USA only)
APPLICANT: Board of Regents, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Prec. ...
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SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
PRILICATION NUMBER: US/08/463,298
FILING DATE: 05-JUN 1995
CLASSIFICATION: 424
PRICA PAPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11060
FILING DATE: 11-NOV-1993
APPLICATION NUMBER: PCT/US93/11060
FILING DATE: 13-NOV-1992
ATTORNEY/AGENT INPORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B173CIP
TELECOMMUNICATION:
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/463,128
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: PCT/US93/11060
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FILING DATE: 13-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 318 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 100.'
Matches 62; Conservative
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08/456,124
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REGISTRATION NUMBER: 35,965
TELEPAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 318 Dasse pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature LOCATION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 100.
Matches 62; Conservative
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STATE: Massachusetts
COUNTRY: USA
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
COTHER INFORMATION:
US-08-822-830B-3
                                                                                                                                                                                                                                                                                                                               LOCATION: 1.318
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
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02109-1875
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LOCATION: 1..3
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APPLICANT: Lobb, Roy R.; Burkly, Linda C.
TITLE OF INVENTION: Treatment for Asthma with VLA-4 Blocking
TITLE OF INVENTION: Agents
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 62; DB 2; Leus-
Pred. No. 1.8e-21;
O: Indels
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APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

BRIOR APPLICATION DATA:

APPLICATION NUMBER:

APPLICATION NUMBER:

BRIOR APPLICATION NUMBER:

APPLICATION NUMBER:

BRIOR APPLICATION NUMBER:

APPLICATION NUMBER:

BRIOR APPLICATION 
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8.5%; Score 62; DB
Best Local Similarity 100.0%; Pred. No. 1.8
Matches 62; Conservative 0; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
                                                                                       RECEIVED NOUNDER: 2/7/74
REFERENCE/DOCKET NUMBER: B173CIP
TELEPHONE: (212) 596-9000
TELEPAX: (212) 596-9000
TELEFAX: (212) 596-9000
TELEFAX: (212) 596-9000
SEQUENCE CHARACTERISTICS:
LENGTH: 318 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08822830B
Patent No. 5871734
   ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35,965
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REGISTRATION NUMBER: 35,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
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STREET: 20
TV. Boston
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432 ATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Lobb, Roy R.; Burkly, Linda C.
TITLE OF INVENTION: Treatment For Inflammatory Bowel Disease
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
                                                                                                                                                                                                                                                       8.5%; Score 62; DB 2; Length 318; 100.0%; Pred. No. 1.8e-21; cive 0; Mismatches 0; Indels
                                                                                                                                             /note= "pBAG172 insert: HP1/2 light chain variable region"
/note= "HP1/2 light chain variable region"
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/950,660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
APPLICATION NUMBER: US 08/373,857
FILING DATE: 18-JAN-1995
BRICK APPLICATION DATA:
APPLICATION NUMBER: US 08/284,603
FILING DATE: 11-AUG-1994
PRICK APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00924
FILING DATE: 02-FEB-1993
PRICK APPLICATION DATA:
APPLICATION NUMBER: US 07/835,139
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: LAHIVE & COCKFIELD
60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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27 ATTCCTGCTTGTTTCAGCAGAACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 86
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APPLICANT: Lobb, Roy R.
APPLICANT: BURKLY, Linda C.
TITLE OF INVENTION:
TITLE OF INVENTION: TREATMENT FOR INFLAMMATORY BOWEL DISEASE
FILE REFERENCE: 10274-004003
CURRENT APPLICATION NUMBER: US/09/157,452B
CURRENT FILING DATE: 1998-09-21
PRIOR APPLICATION NUMBER: US 08/950,660
PRIOR APPLICATION NUMBER: US 08/204,603
PRIOR APPLICATION NUMBER: US 08/204,603
PRIOR APPLICATION NUMBER: US 08/204,603
PRIOR FILING DATE: 1995-01-18
PRIOR PELING DATE: 1995-01-18
PRIOR PELING DATE: 1995-01-20
PRIOR FILING DATE: 1995-02-20
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1993-02-02
PRIOR FILING DATE: 1992-02-12
NUMBER OF SEQ ID NOS: 16
CONTWARE: FASELERQ FOR WINDOWS Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            432 ATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature

LOCATION: 1

COTHER INFORMATION: /note= "pBAG172 insert: HP1/2 light

COTHER INFORMATION: chain variable region"

US-08-950-660-3
                                                                                                                                                                                                                                                                                                                                   /note= "HP1/2 light chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
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8.5%; Score 62; DB 2; Lv
Best Local Similarity 100.0%; Pred. No. 1.8e-21;
Matches 62; Conservative 0; Mismatches 0;
REFERENCE/DOCKET NUMBER: BGP-031USCP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09157452B Patent No. 6482409
                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
                                                               TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
ERNOTH: 318 base pairs
TYPE: nucleic acid
                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                NAME/KEY: CDS
LOCATION: 1..318
OTHER INFORMATION:
OTHER INFORMATION:
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Best Local Similarity
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LENGTH: 318
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                                            FTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 491
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Gaps
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APPLICANT: Carr, Frank J.
APPLICANT: Carr, Frank J.
ITILE OF INVENTION: RECOMBINANT ANTI-VLA4 ANTIBODY MOLECULES
FILE REFERENCE: 10274-007001
CURRENT APPLICATION NUMBER: US/08/454,899G
CURRENT APPLICATION NUMBER: US/08/04/798
PRIOR APPLICATION NUMBER: US 08/004,798
PRIOR PILING DATE: 1993-01-12
PRIOR APPLICATION NUMBER: PCT/US94/00266
PRIOR APPLICATION NUMBER: PCT/US94/00266
SPRIOR SEQ ID NOS: 109
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
TENNOW: 210
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Best Local Similarity 100.0%; Pred. No. 1.8e-21;
Matches 62; Conservative 0; Mismatches 0; Indels
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application PC/TUS9300030
GENERAL INFORMATION:
APPLICANT: Lobb, Roy R.
TITLE OF INVENTION: Treatment for Asthma
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE: OTHER INFORMATION: light chain variable region
0; Mismatches
                                                                                                                                                                                                                                                                          Sequence 9, Application US/08454899G Patent No. 6602503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
62; Conservative
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COMPUTER READABLE FORM:
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; LOCATION: (1)...(318)
US-08-454-899G-9
                                                                                 27 ATTCCTGCTT
                                         432 ATTCCTGCT
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  Matches
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CLASSIFICATION:
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,228
FILING DATE: 15-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Levine, Leslie M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application PC/TUS9410395 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Levine, Leslie M.
REGISTRATION UNDHER: 35,245
REFERENCE/DOCKET UNDHER: D017;
TELECOMMUNICATION INFORMATION:
TELEFONE: (617) 252-9810
TELEFONE: (617) 252-9810
TELEFONE: (617) 252-9617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Leslie M. Levine
STREET: 14 Cambridge Center
CITY: Cambridge
                              LENGTH: 318 base pairs
TYPE: WUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
                                                                                                                                                                                                                                                       NAME/KEY: misc feature LOCATION: 1
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          SEQUENCE CHARACTERISTICS:
LENGTH: 318 base paire
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STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                      NAME/KEY: CDS
LOCATION: 1...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02142
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GENERAL INFORMATION:
APPLICANT: Lobb, Roy R.
TITLE OF INVENTION: Treatment for Inflammatory Bowel Disease
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd.
STREET: 10 South Wacker Drive, Suite 3000
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 318;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: /note= "pBAG172 insert: HP1/2 light
OTHER INFORMATION: chain variable region"
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00924
FILING DATE: 19930202
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: MCNIGholas, Janel M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 92,308-A; D003 CIP PCT
                                                                                                                                     92,307-A; D002 CIP PCT
                                                                                                                                                                                                                                                                                                                                                                                                                          /product= "HP1/2 light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 62; DB 5; L/
Pred. No. 1.8e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

8.5%; Score 62; DB

Best Local Similarity 100.0%; Pred. No. 1.8
  UMBER: PCT/US93/00030
19930112
                                                                                                                                                                                                                                                                                                                                                                                                                                                  variable region"
APPLICATION NUMBER: PCT/US93/0
FILING DATE: 19930112
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MCNICholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 92,30
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 312-715-100
TELEFAX: 312-715-100
TELEFAX: 312-715-103
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
LENGTH: 318 base pairs
TYPE: NUCLEIC ACID
STRANDENNESS: GOUDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 312-715-1234
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 1..318
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                     linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION
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27 ATTCCTGCTTCTAGCAGCAGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 86
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                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                8.5%; Score 62; DB 5; Length 318, 100.0%; Pred. No. 1.8e-21; ive 0; Mismatches 0; Indels
                                                                                                                                                                    LOCATION: 1 - COTHER INFORMATION: /note= "pBAG172 insert: HP1/2 light OTHER INFORMATION: chain variable region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BRORY UNIVERSITY
APPLICANT: GEORGIA TECH RESEARCH CORPORATION
APPLICANT: SWEALLCK, Robert A.
APPLICANT: SWEALLCK, AObert A.
APPLICANT: WICK, Timothy M.
TITLE OF INVENTION: Method of Inhibiting Binding of
TITLE OF INVENTION: Reticulocytes to Endothelium by
TITLE OF INVENTION: Interfering with VLA-4/VCAM-1
TITLE OF INVENTION: Interfering with VLA-4/VCAM-1
TITLE OF INVENTION: Interfering with VLA-4/VCAM-1
TITLE OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leslie M. Levine
LOCATION: 1..318
OTHER INFORMATION: /product= "HP1/2 light chain
OTHER INFORMATION: variable region"
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10395
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432 ATTCCTGCTTGTTTCAGCAGGACAGGGTTACCATAACCTGCAAGGCCAGTCAGAGTGT 491
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                                                                                                                                                                       Query Match 8.5%; Score 62; DB 5; Length 318; Best Local Similarity 100.0%; Pred. No. 1.8e-21; Matches 62; Conservative 0; Mismatches 0; Indels
LENGTH: 318 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLIGY: linear
MOLECTLE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
PCT-US94-10395-2
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87 GA 88
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0; Gaps

Search completed: March 15, 2005, 23:24:20 Job time : 239 secs

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GenCore version 5.1.6
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Title:	US-10-016-686-1
Perfect score:	1279
Sequence:	1 EVQLQQSGPDLVKPGASVKIQQDYNSPPTFGGGTKLEIKR 243
Scoring table: BLOSUM62	BLOSUM62
Gapop 10	Gapop 10.0 , Gapext 0.5
Searched:	2105692 seqs, 386760381 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

2105692

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries A Geneseq 16Dec04:*

1. geneseqp1980s:*

2. geneseqp2000s:*

4. geneseqp2001s:*

5. geneseqp2001s:*

6. geneseqp2003as:*

7. geneseqp2003as:*

8. geneseqp2003bs:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Aaw86002 Murine an	Aay42294 Anti-5T4	Aay27407 5T4 scFv	Aab83835 Amino aci	Aab83838 Amino aci	Aaw86003 Anti-5T4	Aaw86004 Human B7-	Aab83836 Amino aci	Abu07262 Human exp	Abu07253 Human exp	Abp58454 Engineere		Aaw90217 Bispecifi				-				Adg17482 Anti-CD22	•	Aau75369 Diphtheri	Aau75368 Diphtheri	Aau75374 Diphtheri
SUMMARIES		ΙD	AAW86002	AAY42294	AAY27407	AAB83835	AAB83838	AAW86003	AAW86004	AAB83836	ABU07262	ABU07253	ABP58454	ADR70320	AAW90217	AAW90218	ADG17481	AAP80154	ADG17480	ADG17477	AAW82743	AAW82742	ADG17482	ADG17478	AAU75369	AAU75368	AAU75374
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do		Match	100.0	100.0	100.0	100.0	100.0	100.0	99.6	99.66	99.6	99.66	0.94	73.1	70.6	70.2	69.5	69.5	69.3	69.1	69.0	69.0	68.8	68.8	68.7	68.7	68.7
		Score	1279	1279	1279	1279	1279	1279	1274	1274	1274	1274	972.5	935	903.5	897.5	889.5	889	886.5	883.5	883	883	880.5	880.5	879	879	879
	Result	SO.	н	7	m	4	2	9	7	80	σ	10	. 11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

This amino acid sequence comprises an scFv, termed 5T4scFv.1, comprising the heavy chain variable region (VH) from the murine 5T4 monoclonal antibody followed by a 15-amino acid flexible linker and the light chain variable region (VL) of the mouse 5T4 antibody. The trophoblast cell

New vector encoding a tumour interacting protein for treating cancer - contains a desired nucleotide sequence and/or protein which recognises tumours, and is used as a gene delivery system to treat cancer.

WPI; 1999-059910/05.

N-PSDB; AAV80290.

Example 1; Fig 1A; 82pp; English.

_	Aau75367 Diphtheri	Aau75366 Diphtheri	Aau75373 Diphtheri	Aao29672 Anti-T ce	Aao29671 Anti-T ce	Aao29676 Anti-T ce	_	Aao29674 Anti-T ce	Aar05378 Multifunc	Aab62305 Single ch	Adg17484 Anti-CD22	Adf85426 V122scFv	Adg17479 Anti-CD22		Adg17486 Anti-CD22	Abr42054 Newcastle	Adg17487 Anti-CD22	Adg17485 Anti-CD22	Aap80151 Multifunc
AA029673	AAU75367	AAU75366	AAU75373	AA029672	AA029671	AA029676	AAU75375	AA029674	AAR05378	AAB62305	ADG17484	ADF85426	ADG17479	ADG17483	ADG17486	ABR42054	ADG17487	ADG17485	AAP80151
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895	896	968	968	896	968	896	899	899	311	313	244	283	244	244	244	291	244	244	311
68.7	68.7	68.7	68.7	68.7	68.7	68.7	68.7	68.7	9.89	9.89	9.89	68.5	68.5	68.5	68.5	68.3	68.2	68.2	68.0
879	879	879	879	879	879	879	879	879	878	878	877.5	876	875.5	875.5	875.5	874	872.5	872.5	870
56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Tumour interacting protein; cancer, gene therapy; vector; 5T4 antigen; monoclonal antibody; single chain antibody; scFv; mouse; 5T4scFv.1.
                                                                                                                                                                                                                                                  Carroll MW, Myers KA;
                                                     Murine anti-5T4 antigen monoclonal antibody scFv.
                                                                                                                                                                                                                                                  Bebbington CR, Ellard FM,
                                                                                                                                         /note= "encoded by GDT"
                                                                                                                         Location/Qualifiers
        AAW86002 standard; protein; 243 AA
                                                                                                                                                                                                                                    (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                    97GB-00011579.
97GB-00013150.
97GB-00014230.
                                                                                                                                                                                      98WO-GB001627.
                                      15-MAR-1999 (first entry)
                                                                                                                                 Misc-difference 169
                                                                                                                                                                                                     04-JUN-1997;
20-JUN-1997;
04-JUL-1997;
                                                                                                                                                                                                                                                   Kingsman SM,
                                                                                                                                                                                      04-JUN-1998;
                                                                                                                                                        WO9855607-A2
                                                                                                                                                                       10-DEC-1998.
                                                                                           Mus sp.
Synthetic.
Chimeric.
                       AAW86002;
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surface antigen defined by monoclonal antibody 5T4 is expressed at high (see AAV80200) can be used to construct single-chain antibodies (see AAV80200) can be used to construct single-chain antibodies (see AAW80003) and sefv fusion constructs (see AAW80004-05). The invention relates to a vector comprising a nucleotide sequence coding for a tumour interacting protein (TIP) and optionally a nucleotide sequence of interest (NOI) which encodes a protein of interest (POI), the vector being capable of delivering the NOI and/or POI to the tumour recognised by the TIP. Delivery can be in vivo or ex vivo. The vector is used to treat canner, and may also used as a gene delivery system for introducing at least 1 gene encoding a TIP (preferably a tumour binding protein) into a haematopoietic cell lineage
                                                                                                                                                                                                                                                                                                                                                                               NOKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                  61 NQKFKDKALLIVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGGSGGGGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytochrome; targetting; localisation; cancer; tumour; prodrug; reduction;
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                                                                                                                                                                                                                                                                                                                 EVOLOGSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY
                                                                                                                                                                                                                                                                                                                                               1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY
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                                                                                                                                                                                                                                                100.0%; Score 1279; DB 2; Length 243; 100.0%; Pred. No. 7.5e-84; ive 0; Mismatches 0; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-5T4 secreted single chain antibody Fv fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patterson AV, Kingsman SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY42294 standard; protein; 243 AA.
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98GB-00018103.
99GB-00002081.
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N-PSDB; AAZ19786.
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Best Local Similarity
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                                                                                                                                                                                                                  Sequence 243 AA;
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Mitrophanous K;
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19-AUG-1998;
29-JAN-1999;
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This sequence represents an exempte or a secreted single chain antibody of tragment (in this case, directed against the 5T4 antigen), which is involved in transcellular localisation. A secreted single chain antibody of tragment can be fused to optochrome P450 reductase (P450R) derivatives cuch as anchorless P450R (A4742287) or FN fragment (AA742288). This cubbles the fusion protein to be delivered to other cells where it is chen transported to the nucleus. Many drugs' sites of action are in the nucleus, rather than the cytoplasm, where P450R normally functions. P450R or its derivatives can be used to activate prodrugs to their active form via reduction. Administration of a prodrug is useful where the active drug may be metabolised before it reaches its site of action or where the active drug is cytotoxic, e.g., anticancer drugs. Targetted delivery of such prodrug activators allows a reduction in dose of the prodrug, and thus of systems active effects. P450R derivative fusion proteins, or vectors that express them, are specifically used to treat tumours, are specifically used to treat tumours, and muscular dystrophy, but may also be used to read many other conditions, are specifically used to treat tumours, and cathuris, or conditions associated with hypoxia, ischaemia or theumatoid atheritis, or conditions associated with hypoxia, ischaemia or hypoglycemia, or to deliver antibiotics, antiviral agents, analgesics, anti-inflammatories, antineoplastic agents and diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 NÇKFKDKAILITVDKSSTTAYMELRSLISEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                      This sequence represents an example of a secreted single chain antibody
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                    New prodrug activating agent targeted to selected cells or tissues, particularly hypoxic cells, for treating e.g. tumors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1279; DB 2; Length 243; 100.0%; Pred. No. 7.5e-84; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY27407 standard; protein; 243 AA
                                                                                        Example 9; Fig 3; 187pp; English.
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Unidentified

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AAB83835 standard; protein; 243 AA
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AAB83835
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                                                                                                                                                                                                                                                                                       The invention provides a new prodrug activating agent that comprises: (i) a localization domain (LD; other than a tumor-selective antibody) and a prodrug activating domain (RD); (ii) at least one nucleic acid encoding a cytochrome P450 and under control of at least one constitutive or inducible expression control sequence or (iii) a modified hematopoietic stem cell (MHSC) containing at least one nucleic acid encoding a PAD and under control of elements as in (ii). The prodrug activating agent or vectors that express them, are specifically used to treat tumors, inflammation, atherosclerosis and muscular dystrophy, but may also be used to treat many other conditions, e.g. crebral malaria, rheumatoid arthritis, or conditions associated with hypoxia, hypoglycemia or is deliver antibiotics, antivizal agents analgesis, anesthetics, anti-inflammatories, antinosplastic agents and diagnostic agents. LD optimize activity of PAD, e.g. by delivering it to selected ocations or by delivering it to neighboring cells (bystander effect), and allow a reduction in dose of prodrug, and thus of systemic side-frects. Nucleic acids encoding the agent may be expressed selectively in hypoxic cells. The present sequence represents the single chain variable antibody fragment against the tumor antigen 574 (574 scFv): 574 scFv is tuman P450 reductase derivative alP450R
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                                                                                                                                                                                                                               New prodrug activating agent targeted to selected cells or tissues, particularly hypoxic cells, for treating e.g. tumors or inflammation.
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                                                                                                                                                   Griffiths L;
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                                                                                                                                                     Kan 0,
                                                                                                                                                     Patterson AV, Kingsman SM,
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                                                                                                                           (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                      98GB-00018103.
99GB-00002081.
                                                                          98GB-00004841.
                                                  99WO-GB000672
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IKR 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 243 AA;
                                                                                                                                                                 Mitrophanous K;
                                                                                                                                                     Stratford IJ,
  WO9945126-A2
                                                  05-MAR-1999;
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The specification describes the use of a single chain antibody (ScFv), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The ScFv antibody is useful in the manufacture of a disease pharmaceutical composition, for in vivo imaging and/or for advant treatment of a disease. The ScFv antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune diseases, cancers, central nervous system disorders including Parkinson's disease, periodontal diseases, cardiopulmonary diseases, cardiopulmar diseases, cardiopulmonary diseases, cardiopulmar disparse.
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related diseases, and other immune disorders. The present sequence
represents a 514 ScFv of the invention. The antibody comprises the VH and
VL regions from murine 514 monoclonal antibody, joined by a linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
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                                                                                                                                                                                             Single chain antibody; ScFv; inflammatory disease; arthritis; cancer; hypersensitivity; autoimmune disease; central nervous system disorder; Parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovacular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carroll MW, Ellard FM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                     Amino acid sequence of a 5T4 ScFv designated 5T4ScFv.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 1279; DB 4;
100.0%; Pred. No. 7.5e-84;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Ala encoded by GDT"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 3; Fig 1; 118pp; English.
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15-FEB-2000; 2000GB-00003527.
02-MAR-2000; 2000GB-00005071.
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                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200136486-A2
                                                               23-JUL-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAY-2001,
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                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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AAB83835;
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Chimeric.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The specification describes the use of a single chain antibody (ScFV), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The ScFV antibody is useful in the manufacture of a medicament, for affecting a disease in vivo, for preparing a pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The ScFV antibody is also useful for treating inflammatory diseases. The ScFV antibidis, hypersensitivity, autoimmune diseases, cancers, central nervous system disorders including Parkinson's disease, periodontal diseases, cardiovascular
                                         180
                                                                                          240
GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
                                                                                                      Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
                                                                                                                                                                                                                                                                                                                                 Single chain antibody; ScFv; inflammatory disease; arthritis; cancer; hypersensitivity; autoimmune disease; central nervous system disorder; Parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder.
                                                                                        LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ellard FM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bebbington CR, Carroll MW,
                                                                                                                                                                                                                                                                                                          sequence of an Ig-5T4 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Met encoded by CTG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                              AAB83838 standard; protein; 592 AA.
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2000GB-00003527.
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                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                   243
                                                                                                                                         IKR 243
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Misc-difference
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 diabetes, Helicobacter-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New vector encoding a tumour interacting protein for treating cancer - contains a desired nucleotide sequence and/or protein which recognises tumours, and is used as a gene delivery system to treat cancer.
                                                                                                                                                                                                                                                                                                                      140 GGGSGGGGGGGGSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT
                                                                                                                                                                                                                                                                                                                                                                                    200 LLISYISSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE
                                                                                                                                                                                                                                                                  80 NOKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS
                                                                                                                                                                                                                                                                                                    121 GGGGSGGGGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT
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                                                                                                                                                                     1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY
                                                                                                                                                                                                    20 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY
                                                                                                                                                                                                                                     NOKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS
                                                                                                                                      Gaps
diseases, gastrointestinal disorders, infections, diabetes, Helicol related diseases, and other immune disorders. The present sequence represents an Ig-5T4 fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tumour interacting protein; cancer; gene therapy; vector; 5T4 ant:
monoclonal antibody; single chain antibody; mouse; human; 5T4Sabl
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                                                                                                     Length 592;
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                                                                                                   100.0%; Score 1279; DB 4;
100.0%; Pred. No. 2e-83;
ive 0; Mismatches 0;
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97GB-00014230.
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                                                                                                                     Local Similarity 100.
1es 243; Conservative
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                                                                      Sequence 592 AA;
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Synthetic.
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5T4Sabl, comprising an scFv derived from murine monoclonal antibody 5T4 (see AAW86022) and the human gl constant region. CDNA (see AAV80221) encoding the Sab has been inserted into vector pCineo to allow expression in mammalian cells. The trophoblast cell surface antigen defined by 5T4 is expressed at high levels on the cells of a wide variety of human tumnours. The invention relates to a vector comprising a nucleotide sequence coding for a tumour interacting protein (TIP) and optionally a nucleotide sequence of interest (NOI) which encodes a protein of interest (POI), the vector being capable of delivering the NOI and/or POI to the tumour recognised by the TIP. Delivery can be in vivo or ex vivo. The vector is used to treat cancer, and may also used as a gene delivery system for introducing at least 1 gene encoding a TIP (preferably a tumour binding protein) into a haematopoietic cell lineage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240
                                                                                                                                                                                                                                                                                                                                                   NOKPKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5T4 antigen;
B7-1;
                                                                                                                                                                                                                                                                                                                 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY
                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                 100.0%; Score 1279; DB 2; Length 595; 100.0%; Pred. No. 2e-83; cive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumour interacting protein; cancer; gene therapy; vector; monoclonal antibody; single chain antibody; mouse; human; co-stimulatory molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human B7-1.5T4.1 protein fusion, specific for human 5T4.
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97GB-00014230.
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                                                                                                                                                                                                         Sequence 595 AA;
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Synthetic.
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This is the amino acid sequence of .B7-1.5T4.1, a fusion protein

comprising the extracellular domain (amino acids 1-215) of human co-
stimulatory molecule B7-1 joined via a flexible peptide linker to an scro
(see AAW86022) derived from murine 5T4 monoclonal antibody. B7-1.5T4.1

contact (see AAW86022) can be inserted into vector pCI to allow expression

of the fusion protein in mammalian cells. The trophoblast cell surface
antigen defined by 5T4 is expressed at high levels on the cells of a wide

variety of human tumours. The invention relates to a vector comprising a

nuclectide sequence coding for a tumour interacting protein (TIP) and

optionally a nucleotide sequence of interact (NOI) which encodes a

protein of interest (POI), the vector being capable of delivering the NOI

cor and/or The vector is used to treat cancer, and may also used as a

gene delivery system for introducing at least I gene encoding a TIP

(preferably a tumour binding protein) into a haematopoietic cell lineage.

Chreterably a tumour binding protein) into a haematopoietic cell lineage.

T-cells
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                                                                        New vector encoding a tumour interacting protein for treating cancer - contains a desired nucleotide sequence and/or protein which recognises tumours, and is used as a gene delivery system to treat cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 EVÖLĞĞĞGPDLVKPÇASVKISCKASĞYSFTĞYYMHWVKQSHĞKSLEWIGRINPNNGVTLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.6%; Score 1274; DB 2;
100.0%; Pred. No. 3.7e-83;
ive 0; Mismatches 0;
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                                                                                                                                                       Example 5; Fig 2; 82pp; English
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                                   N-PSDB; AAV80292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 488 AA;
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Synthetic

Mus sp.

Carroll MW, Myers KA;

Kingsman SM,

Human expressed protein tag (EPT) #1963.

(first entry)

28-MAR-2002; 2002WO-US009671.

WO200278524-A2. 10-OCT-2002

Ношо

04-DEC-2001; 2001US-0336780P. 20-FEB-2002; 2002US-0358985P

Tomlinson AJ,

Chicz RM,

(ZYCO-) ZYCOS INC.

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Translational profiling; expressed protein tag; EPT; kinase; phosphatase protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MKC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.
                                                                                                                                                                                                                                                              28-MAR-2001; 2001US-0279495P.
21-MAY-2001; 2001US-0292544P.
08-AUG-2001; 2001US-0310801P.
01-OCT-2001; 2001US-0326370P.
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                                                                                                                                                                                          Kingsman A; Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                       Use of single chain antibody capable of recognizing a disease molecule for manufacturing a medicament for preventing and/or disease condition associated with disease associated molecule.
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Pred. No. 3.7e-83;
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100.0%; Pred. No. 5...
... 0; Mismatches
                                                                                                                                                              (OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                English
                                                                                                       18-NOV-1999; 99WO-GB003859.
15-FEB-2000; 2000GB-00003527.
02-MAR-2000; 2000GB-00005071.
                                                                              13-NOV-2000; 2000WO-GB004317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 242, Conservative
                                                                                                                                                                                                                                                                                                                               Claim 3; Fig 2; 118pp;
                                                                                                                                                                                                                                  WPI; 2001-343805/36
                                                                                                                                                                                                                                                N-PSDB; AAF89730
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                           WO200136486-A2
 Homo sapiens
                                                      25-MAY-2001
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The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The polypeptide is useful for trading cancer. The polypeptide is also useful for trading cancer. The polypeptide is also useful for trading polypeptide. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polymucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an treating the above mentioned diseases. This sequence represents an profiling. Note: This sequence does not appear in the printed profile and the printed profile and the printed and the pri
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100.0%; Pred. No. 3.7e-83;
ive 0; Mismatches 0;
Example 2; SEQ ID NO 1963; 134pp; English.
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ABU07262 standard; protein; 488 AA.

ABU07262

ABU07262 ID ABU0 XX AC ABU0

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Query Match
Best Local Similarity
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Sequence 488 AA;
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fragment of a kinase, phosphatase, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide; or the antibody that binds to this polypeptide. The purified polypeptide, or the antibody that binds to this useful for treating cancer. The polypeptide is also useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MRC-binding polypeptide. The polypeptides and polymentally useful for treating or preventing polymentally useful for treating or preventing implema, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expension that sequence does not appear in the printed cormat directly from WIPO at the wipo int/pub/published_pct_sequences
 367 GGGGSGGGGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 426
                                      Translational profiling; expressed protein tag; BPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatability complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
                       LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention describes a purified polypeptide, which comprises a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 2; SEQ ID NO 1954; 134pp; English.
                                                                                                                                                                                                                                          Human expressed protein tag (EPT) #1954
                                                                                                                                                                ABU07253 standard; protein; 488 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Urban
                                                                                                                                                                                                                                                                                                                                                                                                                                              28-MAR-2001; 2001US-0279495P.
21-MAY-2001; 2001US-0292544P.
08-AUG-2001; 2001US-0310801P.
04-DCT-2001; 2001US-0326370P.
04-DEC-2001; 2001US-0336780P.
20-FEB-2002; 2002US-0356985P.
                                                                                                                                                                                                                                                                                                                                                                                                                         28-MAR-2002; 2002WO-US009671
                                                                                                                                                                                                                 (first entry)
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                                                                          IK 242
                                                                                                 İK 488
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                                                                                                                                                                                               NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
                                                                                                                                                                                                                                                                                                                                             367 GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT.426
                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                   247 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY
                                                                                                                                                                                                                                           307 NOKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS
                                                                                                                                                                                                                                                                                              121 GGGGSGGGGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPŢ
                                                                                                                                                                                                                                                                                                                                                                                              LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE
                                                                                             1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Superantigen, staphylococcal enterotoxin, antibody, cancer, tumour, cytostatic, vaccine, human, SEA/E-120, mutant, mutein.
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Length 488;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note= "wild-type His substituted by Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "wild-type Arg substituted by Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "wild-type Asn substituted by Thr"
                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note= "wild-type Val substituted by
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "wild-type Lys substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note= "wild-type Ser substituted by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |21. .222
|note= "C242 constant heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "wild-type Ser substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "5T4 variable heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Engineered superantigen for human cancer therapy.
99.6%; Score 1274; DB 6; 100.0%; Pred. No. 3.7e-83;
            100.0%; Pred. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABP58454 standard; protein; 672 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               226. .458
/note= "SEA/E-120"
                                                 Matches 242; Conservative
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181 LYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDSGGPSEKSEEINEKDLRKK 240

121 AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD

120

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120

241 SELQGTALGNLKQIYYYNSKAITSSEKSADQFLTNTLLFKGFFTGHPWYNDLLVDLGSTA 300

301 ATSEYEGSSVDLYGAYYGYQCAĞGİPNKTACMYĞÖVTLHDNNRLTEEKKVPINLWIDGKQ 360

NOKFKDKATLTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGOGTSVTVSS 120

420 157 480 217 540

361 TTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRGLIVFHSSEGSTVS

133

135

481 CKASQSVSNDVAWYQQKPQQSPKLLISYTSSRYAGVPDRFSGSGYGTDFTLTISSVQAED

158

CKASQSVSNDVAWYQQKPGQSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAED

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Conjugate for therapy, has bacterial superantigen with a region in T-cell receptor and four regions to determine binding to class II major histocompatibility complex, antibody to cancer associated cell surface structure.
                                                                              Ser
                                                                                                                                                         Ser"
                                                                                                                                   note= "wild-type Phe substituted by Leu"
/note= "wild-type Lys substituted by Ser"
                                                                           note= "wild-type Phe substituted by
                                                                                                                                                       /note= "wild-type Thr substituted by
                                                                                                                 'note= "wild-type Ile substituted by
                                                                                                                                                                          'note= "wild-type Leu substituted by
                                                                                                                                                                                     /note= "wild-type Leu substituted by 566. .672
                   'note= "wild-type Lys substituted
                                      substituted
                                                                                                substituted
                                                                                                                                                                                                     566. .672
/note= "C242 constant light chain"
                                                                                                                                                                                                                                                                                                                                 Walse B;
                                               459. .565
/note= "5T4 variable light chain"
                                                                                                                                                                                                                                                                                                                                 Antonsson P,
                                     'note= "wild-type Asp
                                                                                               'note= "wild-type Thr
                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; Fig 10; 102pp; English
                                                                                                                                                                                                                                                                        19-JUN-2002; 2002WO-SE001188
                                                                                                                                                                                                                                                                                           28-JUN-2001; 2001SE-00002327
                                                                                                                                                                                                                                                                                                                                Erlandsson E,
                                                                                                                                                                                                                                                                                                              (ACTI-) ACTIVE BIOTECH AB
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          Misc-difference
                            Misc-difference
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                                                                                                                                                                                                                                                                                                                                Forsberg G,
                                                                                                                                                                                                                                                      09-JAN-2003
                                                Region
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of the following amino acid substitutions to reduce seroreactivity whilst maintaining production levels and biological activity: R20G, N31T, S24G, R27K, K79E, K81E, K83S and D227S. SEA/E-120 was geneticially fused to the Fab moiety of the tumour reactive antibody 574. Substitutions were made in the 574 sequence to obtain higher yields: in the heavy chain, H41P, 844G, 169T and V113G; and in the light chain, F10S, T45K, 163S, F73L, T77S, L78V and L63A. An expression vector comprising DNA encoding the conjugate can be used to transform host cells for recombinant production of the conjugate. The conjugate is useful for treating cancer, including cancer of the lung, breast, colon, kidney, pancreas, ovary, stomach, The present sequence is a conjugate of a bacterial superantigen and an antibody moiety, and has been designed to target and destroy cancer cells. The bacterial superantigen is SEA/B-120 (see also ABS6855), which was derived from staphylococcal enterotoxin B (SEB) by the incorporation

Sequence 672 AA;

Indels 323; ch 76.0%; Score 972.5; DB 6; Length 672; 11 Similarity 40.1%; Pred. No. 2.1e-61; 227; Conservative 3; Mismatches 13; Indels 323. Query Match Best Local Si Matches 227,

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EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY

WPI; 2004-652917/63. N-PSDB; ADR70322 NOKFKDKALLTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVS- 119 9

New molecules that modulate poliovirus receptor (PVR) mediated adhesion, receptor mediated adhesion modulation; cell trafficking behaviour modulation; cell invasion behaviour modulation; proliferative disorder; cancer; metastasis; PVR-mediated adhesion; PVR-mediated invasion potential; ä receptor; PVR; CD155; cluster of differentiation 155; Jay Torella C, Poliovirus receptor (PVR)-specific scFv2 protein. Lain B, 243 541 AAVYFCQQDYNSPPTFGGGTKLEIKR 566 218 LAVYFCQQDYNSPPTFGGGTKLEIKR Zehetmeier C, ADR70320 standard; protein; 267 24-FEB-2003; 2003US-0450064P. 28-MAY-2003; 2003EP-00012314. 19-FEB-2004; 2004WO-EP001637 (first entry) (XERI-) XERION PHARM AG. Beste G, Zo , Sloan KE; TUFT) UNIV TUFTS WO2004074324-A2. Unidentified 18-NOV-2004 Eustace BK, 02-SEP-2004 poliovirus ADR70320; Jnger CM, RESULT 12 ADR70320 ò

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119
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                                                                                                                                          intra- or extracellular domain of the poliovirus receptor (PVR) - also known as CD155 (cluster of differentiation 155). The molecules of the invention have the ability to modulate receptor mediated adhesion, trafficking and/or invasion behaviour of a cell expressing PVR. The molecules of the invention are useful for the prevention and/or treatment of proliferative disorders, cancer or metastasis. The molecules of the invention are also useful for identifying agents that can modulate PVR-mediated adhesion or invasion potential of cells. The present amino acid sequence represents a PVR-specific scFv protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 KFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSSGG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 GGSGGGGGGGSS--IVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNS-PPTFGGGTKL 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60
                                                                                                                           The invention comprises molecules that specifically bind to at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86; T cell activation; inhibitor; graft versus host disease; transplant rejection; allograft rejection; autoimmune disease; therapy; human; bispecific tetravalent antibody; BiTAb; BiTAb;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 QLQQSGPELVKPGASVKISCKTSGYTPTEYTMHWVKQSHGKSLEWIGGIHPNNGDTSYNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 OLOOSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLYNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
trafficking and/or invasion behavior of a cell expressing CD155 or useful for preventing or treating proliferative disorders, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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                                                                                                                                                                                                                                                                                                                                                                                               73.1%; Score 935; DB 8; Length 267; 76.1%; Pred. No. 3.8e-59; ive 19; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bispecific tetravalent antibody BiTAbB7-24-IG10H6.
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/note= "VH region anti B7.1 MAb"
1139. .153
/note= "(G4S3) flexible linker"
154. .262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "pelB signal peptide"
                                                                                  Claim 7; SEQ ID NO 4; 87pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                           Sequence 267 AA;
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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This polypeptide comprises the bispecific tetravalent antibody BiTAbB7-24

"1G10H6. The molecule consists of 4 scFvs, i.e. 2 anti B7.1 scFvs and 2

"1G10H6. The molecule consists of 4 scFvs, i.e. 2 anti B7.1 scFvs and 2

"1G10H6. The molecules, each containing both an anti B7.1 and anti B7.2 scFv

"1G10H6. The molecules, each containing both an anti B7.1 and anti B7.2 scFv

"1G10H6. The anti-B7.1 and and anti-B7.2 scFv are linked using a charactarion domain (see AAMOG19), which drives the homodimentation of the molecule. DNA (see AAMOG19), which drives the homodimentation of the BITAb in transformed E. coli cells. The BITAD cross-links, and/or cross-reacts, with the costimulatory molecules B7.1 and B7.2 that are expressed on the membrane of professional antigen-

"The invention relates to such B7-binding molecules, methods activation. The invention relates to such B7-binding molecules, methods continent production, and their use for treating or preventing diseases

"The immune system, in particular graft rejection, graft versus host disease, allergy and autoimmune diseases (claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                          /note= "codons for these amino acids are not present in the DNA sequence for BTiTAbB7-24-1G1-H6 provided in the specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  325 QVQLQQSGPELEKPGASVKISCKASGYSFTGHNYMYVKQSNGKSLEWIGIIDPYYGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          385 NPKFEGKATLTVDKSSSTAYMQLESLTSEDSAVYYCARFAYYGDYYYIMDYWGQGTTVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 NOKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITN--YVMDYWGQVTSVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 BVOLOOSGPDLVKPGASVKISCKASGYSFTGYYMHWVKOSHGKSLEWIGRINPNNGVTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New molecules which bind B7.1 and B7.2 - useful to prevent and treat immune diseases including allograft rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
6
                                                                                                                                                                                                     note= "helix-turn-helix dimerisation domain"
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                                                                                                                                                                                                                                                              320. .446
//note= "VH region anti B7.2 MAb"
note= "VL region anti B7.1 MAb"
                                                                                                                                    note= "human IgG3 hinge region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'note= "VL region anti B7.2 MAb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "(G4S3)flexible linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bosman A;
                                                                    note= "encoded by CTG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 7.1; Fig 16; 182pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "His6 tag'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-EP003791.
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                                                                                                                                                                    .308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-105615/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAX01651
                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 580 AA;
                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JUN-1998;
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233 564

445 173 AAW90218;

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This polypeptide comprises the bispecific tetravalent antibody BiTAb1G10-B7-24H6. The molecule consists of 4 scFvs, i.e. 2 anti B7.1 scFvs and 2 anti B7.2 scFvs (tetravalency). One single BiTAb is a homodimer of 2 identical molecules, each containing both an anti B7.1 and anti B7.2 scFv (bispecificity). An anti-B7.1 and and anti-B7.2 scFv are linked using a charactation domain (see AAW90219), which drives the homodimerisation of the molecule. DNA (see AAW90219) unit and scheen constructed to allow expression of the BiTAb in transformed E. coli cells. The BiTAb cross-links, and/or cross-reacts, with the costimulatory molecules B7.1 and B7.2 that are expressed on the membrane of professional antigency reseming cells, leading to the inhibition of antigen-specific T cell activation. The invention relates to such B7-binding molecules, methods of the immune system, in particular graft rejection, graft versus host disease, allergy and autoimmune diseases (claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GGGGSGGGGGGGSGIVMTQTPTFLLVSAGDRVTITCKASQSV-----SNDVAWYQQK 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PGQSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFG 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 QLQQSGPELEKPGASVKISCKASGYSFTGHNMNWVKQSNGKSLEWIGIIDPYYGGTSYNP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                        3 QLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLYNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITN--YVMDYWGQVTSVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-CD22 antibody; antibody; humanised anti-CD22 antibody; immunoconjugate; malignant B cell growth inhibition; cytostatic; lymphoma; B cell non-Hodgkin's lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Anti-CD22 antibody related variant MLV 11.2 protein SEQ ID NO:6.
                                                                                                                                                                                                                                                                                                                                                                     DB 2; Length 556;
                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                               70.2%; Score 897.5; DB 2; 71.9%; Pred. No. 4.2e-56; ive 26; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
         Example 7.1; Fig 18; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADG17481 standard; protein; 244 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rybak S, Arndt M, Krauss J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-2002; 2002US-0387306P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JUN-2003; 2003WO-US018201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 71.9
Matches 179; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 GGTKLEIKR 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 GGTKLEIKR 248
                                                                                                                                                                                                                                                                                                                               Sequence 556 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003104425-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-DEC-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
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                                                                                              563
                                                                                                                                                                                                                                                                                                                                                                                         B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86; T cell activation; inhibitor; graft versus host disease; transplant rejection; allograft rejection; autoimmuse disease; allergy; therapy; human; bispecific tetravalent antibody; BiTAb; BiTAb;
QKPGQSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New molecules which bind B7.1 and B7.2 - useful to prevent and treat immune diseases including allograft rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "helix-turn-helix dimerisation domain"
                                                                                                                                                                                                                                                                                                                                                           Bispecific tetravalent antibody BiTAb1G10-B7-24H6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "VH region anti B7.2 MAb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "VL region anti B7.2 MAb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "human IgG3 hinge domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B7.1 MAD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           306. .426
/note= "VH region anti B7.1 MAb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "human IgG3 hinge region'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "(G4S3) flexible linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'note= "(G4S3)flexible linker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bosman A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              442. .550
/note= "VL region anti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                   AAW90218 standard; protein; 556 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "His6 tag"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-EP003791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97EP-00870092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "b"-
                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .135
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                                                                                                                                                    FGGGTKLEIKR 574
                                                                                                                              FGGGTKLEIKR 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sablon E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-105615/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAX01652.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                                                                                                        10-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JUN-1998;
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Chimeric

Mus sp.

Peptide

Region Region Domain Domain Region

Key Region

Peptide

Peptide

Region

Lorre K,

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Gaps

6

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The present invention describes a stable anti-CD22 antibody having a VH domain and a VL domain, where the sequences of the VH and VL domains are at least 70% to 90% identical to the a sequence of 244 amino acids at DaG17476) and the antibody comprises at least two amino acid substitutions with respect to ADG17476, Gln replacing Glu at position 6, Val replacing Ser at position 12 or Lys replacing Glu at position 6, the VH domain. Also described: (1) an isolated mucleic acid encoding a stable humanised anti-CD22 antibody described above and that has an LL2 binding specificity; (2) an immunoconjugate comprising a stable anti-CD22 antibody described above; (3) a mucleic acid encoding an immunoconjugate of (1); (4) a method of inhibiting growth of a malignant B cell; and (5) a method of detecting a cell that expresses CD22. The anti-CD22 antibody. has cytostatic activity. The antibodies are useful in diagnosing or treating lymphoma, e.g. B cell non-Hodgkin's lymphoma. The present carding the exemplification of the present invention.
                                                                                                    New anti-CD22 antibody having a VH domain and a VL domain comprising at least two amino acid substitutions, useful in diagnosing or treating lymphoma, e.g. B cell non-Hodgkin's lymphoma.
                                                                                                                                                                                                            Disclosure; SEQ ID NO 6; 66pp; English
                         WPI; 2004-062346/06.
N-PSDB; ADG17493.
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Sequence 244 AA;

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NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
                                                                                                           61 NQKFKDKATLTADKSSSTAYMQLSSLTSEDSAVYYCARRDITT----FYWGQGTTLTVSS 116
                                                                                                                                           GGGGGGGGGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSV-----SNDVAWYQQK 174
                                                                                                                                                        9
                                                              1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY
                         11;
  69.5%; Score 889.5; DB 8; Length 244; 69.9%; Pred. No. 6.3e-56; ive 27; Mismatches 37; Indels 11;
Query Match
Best Local Similarity 69.9°
Matches 174; Conservative
                                                                                                                                                                                                                                       GGTKLEIKR 243
                                                                                                                                                                                                                                                     236 GGTKLEIKR 244
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Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

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NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMI-TNYVMDYWGQVTSVTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 BVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 38, Application US/09423439

Patent No. 6339070

Batent No. 6339070

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: CHEMICAL COMPOUNDS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

NUMBER OF SEQUENCES: 6

CORPETET: 1100 New York Ave., N.W.

CITY: Washington

CITY: Washington

CITY: Washington

COMPUTER: D.C.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: ISM Word

CURRENT APPLICATION NUMBER: US/09/423, 439

FILING DATE: 09-NO. 6339070-1999

CLASSIFTCATION: CURMONN:

PRIOR APPLICATION NUMBER: CT/GB98/01294

FILING DATE: 05-MAY-1998

APPLICATION NUMBER: GB 9709421.3

FILING DATE: 05-MAY-1997

INPORMATION FOR SEQ ID NO: 38:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69.0%; Score 883; DB 3; L. 67.6%; Pred. No. 5.4e-70; ive 38; Mismatches 35;
                                  US-09-526-738A-4
US-08-25-838-16
US-08-46-4738-16
US-08-800-198-8
US-08-800-198-8
US-08-840-713-2
US-08-840-713-35
US-08-840-713-37
US-08-25-838-14
US-08-25-838-14
US-08-465-4738-7
US-08-465-4738-7
US-08-465-4738-1
US-08-465-4738-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 288 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 67.6
Matches 169; Conservative
US-09-423-439-38
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Compugen Ltd
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US-09-423-439-32
US-08-419-788-30
US-09-419-788-30
US-09-070-408-132
US-09-070-408-132
US-10-095-246-35
US-10-095-246-35
US-10-095-246-37
US-10-095-246-37
US-10-095-246-37
US-10-095-246-37
US-10-095-246-37
US-08-553-497A-20
US-08-553-497A-24
US-08-553-497A-24
US-08-553-497A-24
US-08-1386-4
US-08-461-8386-4
US-08-461-8386-4
US-08-461-8386-4
US-08-853-497A-22
US-08-861-341-5
US-08-861-341-5
US-08-861-341-5
US-08-861-341-5
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                       version :
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Maximum Match 100%
Listing first 45 summaries
                                                                                                     protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                     GenCore
Copyright (c) 1993
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seq length: 200000000
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1279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 NGKFKGKATLÍTADRSSSTAYMQLSSLÍTSVGSÁVYFCAKENNRFDERGYYAMDÝWGÓGÍTV 123
                                                                                                                                                                                                                                                                                             APPLICANT: Fleer, Reinhard
APPLICANT: Fournier, Alain
APPLICANT: Guitton, Jean-Dominique
APPLICANT: Guitton, Jona, Jean-Dominique
APPLICANT: Veh, Patrice
APPLICANT: Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 31-JAN.1992

FRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN.1993
ATTORNEY/ACENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
REFERENCE/DOCKET NUMBER: ST92006-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
                                                                                                                                                                                                                            Sequence 18, Application US/08797689
Patent No. 5876969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION
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COMPUTER: Macinicos...
COPERATING SYSTEM: System
COPERATING SYSTEM: NATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (610) 454-3839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhone-Poulenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 500 Arcola Road, CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (610) 454-3808
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                         234 GGGTKLEIKR 243
                                                                                                         259 GGGTKLEIKR 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-797-689-18
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Pou
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                                                                                83 NEKFKNKATLTVDKSSTTAYMQLSSLTSEDSAVYYCARERAYGYDDAMDYWGQGTTVTVS 142
                                                    120 SGGGGSGGGGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSND------VAWYQQ 173
                                                                                                                                                 KPGOSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTF 233
                                                                                                                                                                                 61 NQKFKDKAILTVDKSSTTAYMELRSLISEDSAVYYCARSTMI-TNYVMDYWGQVTSVTVS 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     120 SGGGGGGGGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSND-----VAWYQQ 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 BVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY
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67.6%; Pred. No. 1.6e-69;
tive 38; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Pillsbury Winthrop, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
PPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
NN FOR SEQ ID NO: 32:
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32, Application US/09423439
Patent No. 6339070
GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-No. 6339070-1999
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1100 New York Ave., N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-09-423-439-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 673 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 67.6
Matches 169; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A. ZIP: 20005
                                                                                                                                                                                                                                                GGGTKLEIKR 243
                                                                                                                                                                                                                                                                                          GGGTKLEIKR 271
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61 NQKFKGKATLIYDKSSSTAYMQLNSLTSEDSAVYYCA---VGGNYVDWFAYWGQGTLVTV 117
                                                                                                                           117 TVSSGGGGGGGGGGGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 SSGGGGGGGGGGGGSSIVMTQTPTLLVSAGDRVTITCKASQSV--SND---VAWYQQ 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124 TVSSGGGGGGGGGGGGGSNIQLTQSPNSMSTSVGDRVSITCKASQDVDTSVAWYQQKPG
                                                                                                                                                                                                                                            4 QVQLEQSGPELVKPGASVKISCKASGYAFSRSWMNWVKQRPGQGLEWIGRIYPGDGDTKY
                                             NOKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITN----YVMDYWGQVTSV
                                                                   64 NGKFKGKATLTADRSSSTAYMQLSSLTSVGSAVYFCAKENNRFDERGYYAMDYMGQGTTV
                                                                                                                                                                                                                   QSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SCHILLBERG, Stefan
APPLICANT: SCHILLBERG, Stefan
APPLICANT: SCHILLBERG, Stefan
APPLICANT: MARING, Jorg
APPLICANT: Markus
APPLICANT: SACK, Markus
APPLICANT: ENGR.
APPLICANT: ENGREL, Holger
APPLICANT: ENGREL, Holger
APPLICANT: ENGRE, Molecular Pathogenicide Mediated Plant Disease
TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
TITLE OF INVENTION: Realstance
FILE REPERENCE: 0147-0189P
CURRENT APPLICATION NUMBER: US/09/419,788
CURRENT FILING DATE: 1999-10-18
EARLIER APPLICATION NUMBER: 98 11 9630.6 EP
EARLIER APPLICATION NUMBER: 66/BOM/1998 INDIA
EARLIER PILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EVOLOQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY
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OTHER INFORMATION: Description of Artificial Sequence: synthetic,

CTHER INFORMATION: natural origin
US-09-419-888-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 67.1%; Score 858; DB 4; Best Local Similarity 69.2%; Pred. No. 7.9e-68; Matches 173; Conservative 24; Mismatches 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 30, Application US/09419788 Patent No. 6825325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                      237 TKLEIK 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES
QSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGG 236
                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.3%; Score 861; DB 4; Length 249; 67.9%; Pred. No. 3.9e-68; ive 28; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: FR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: ST92006-US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Rhone-Poulenc Rorer Inc
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-Oct-2001
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-984-186-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P-38,619
                                                                                                                                                                                                                                                                                                                                                                                          Fournier, Alain
Guitton, Jean-Dominique
Jung, Gerard
Yeh, Patrice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (610) 454-3839
                                                                                                                                                                                                                                                                                                    Sequence 18, Application US/09984186
Patent No. 686819
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19426
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 249 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 67.99
Matches 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
                                                                                                                                                    237 TKLEIK 242
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244 TKLEIK 249
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1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY

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62 NQKFKGKATLITVDKSSSTAYMELRSLISEDSAVYYCAGSSG-NKWAMDYWGHGASVIVSS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 GGGGSGGGGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSV--SND---VAWYQQKP 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          176 GQSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGG 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 BVQLQQSGPELVKPGASVRMSCKSSGYIFTDFYMNWVRQSHGKSLDYIGYISPYSGYTGY 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY
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                                                                                                                                                                                                                                                            APPLICANT: Iverson, Brent L.
APPLICANT: Georgiou, George
APPLICANT: Burks, Blizabeth A.
ITILE OF INVENTION: IN VITEO SCANNING SATURATION MUTAGENESIS
TITLE OF INVENTION: OF PROTEINS
NUMBER OF SEQUENCES: 132
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match 66.3%; Score 848; DB 3; Length 269; Best Local Similarity 67.3%; Pred. No. 6e-67; Matches 167; Conservative 32; Mismatches 43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,408
FILING DATE: CONCURTENTLY Herewith
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/045,409
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: MCM11lian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REGISTRATION NUMBER: P-43,363
REGISTRATION NUMBER: UTSB:593
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
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TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECHOME: 511/418-3000
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                                                                                                                                                                                                   Sequence 132, Application US/09070408
Patent No. 6180341
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 132: SEQUENCE CHARACTERISTICS:
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512/447-7577
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MEDIUM TYPE: Floppy
                                                               236 GTKLEIKR 243
                                                                                                  240 GTKLELKR 247
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STATE: Texas
COUNTRY: USA
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US-09-070-408-132
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                                                                                                                                                                                           APPLICANT: Tresson, Brent
APPLICANT: Georgiou, George
APPLICANT: Georgiou, George
APPLICANT: Chen, Gang
TITLE OF INVENTION: INTRODES USING CELL SURFACE EXPRESSED
TITLE OF INVENTION: LIBRARIES
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: P. O. Box 4433
CITY: Houston
                                                                                                                                      Sequence 1, Application US/08447402
Patent No. 5866344
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 1:
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amino acid
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                     234 GGGTKLEIKR 243
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## Sequence 35, Application US/10096246A
## Sequence 35, Application US/10096246A
## Patent No. 6818748
## GENERAL INFORMATION:
## APPLICANT: Fulton, R. Elaine
## APPLICANT: Alvi, Azhar 2.
## APPLICANT: Alvi, Azhar 2.
## APPLICANT: Alvi, Azhar 2.
## APPLICANT: Alvi, Azhar 2.
## APPLICANT: Alvi, Azhar 2.
## APPLICANT: Alvi, Azhar 2.
## APPLICANT: Alvi, Azhar 2.
## APPLICANT: Nagata, Leslie
## APPLICANT: Nagata, Leslie
## APPLICANT: Nagata, Leslie
## APPLICANT: Nagata, Leslie
## APPLICANT: Nagata, Leslie
## APPLICANT: Alvi, Azhar 2.
## APPLICANT: US. 10/096,246A
## CURRENT APPLICATION NUMBER: US. 10/096,246A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 NOKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS
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                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-35
CURRENT APPLICATION NUMBER: US/10/092,246
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 37
SSOTWARE: PatentIn version 3.1
SSO ID NO 35
LENGTH: 240
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Patent No. 6501314
GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT:
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                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09486814A

| Patent No. 6562590
| GENERAL INFORMATION:
| APPLICANT: HAYASHI, No. 65625910
| APPLICANT: HAYASHI, No. 65625910
| APPLICANT: TAMAMOTO, Hiroko
| APPLICANT: TAMAMOTO, Hiroko
| APPLICANT: TAMAMOTO, Hiroko
| TITLE OF INVENTION: SINGLE-CHAIN ANTIBODY AGAINST HEPATITIS B VIRUS CORE
| TITLE OF INVENTION: PROTEIN, GENE THEREOF, AND THERAPEUTIC AGENT FOR
| TITLE OF INVENTION: HEPATITIS B CONTAINING THESE
| TITLE OF INVENTION: HEPATITIS B CONTAINING THESE
| TITLE REPERENCE: 0020-4662P
| CURRENT APPLICATION NUMBER: US/09/486,814A
| CURRENT FILING DATE: 202-06-13
| NUMBER OF SEQ ID NOS: 14
| SSOFTWARE: Patentin Ver. 2.1
| SEQ ID NO 2
| LENGTH: 297
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LOCATION: (1)..(145)
OTHER INFORMATION: Identification Method:
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; OTHER INFORMATION: Identification Method:
US-09-486-814A-2
                                                             241 GTKLEIIR 248
    GTKLEIKR 243
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US-10-092-246-35
    236
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61 NOKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
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                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                        51; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: KORT, Alex A.
APPLICANT: IRVING, Robert A.
APPLICANT: ATWALBL, John L.
APPLICANT: MALBY, Robyn L.
APPLICANT: POWER, Barbara E.
APPLICANT: COLMAN, Peter M.
TITLE OF INVENTION: TARGET BINDING POLYPEPTIDE
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                   65.2%; Score 833.5; DB 4 66.3%; Pred. No. 9.9e-66; Live 26; Mismatches 51
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FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
PRICH APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU93/00491
FILING DATE: 24-SEP-1993
PRICH APPLICATION DATA:
APPLICATION NUMBER: AU PL 4973
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: BERY, SCEPHON A.
REGISTRATION NUMBER: 29,768
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
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STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
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Patent No. 5844094
                                                                                                                                                                                                       Query Match
Best Local Similarity 66.3<sup>3</sup>
Matches 161; Conservative
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                                                TYPE: PRT
ORGANISM: mouse
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US-08-403-853-18
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Sequence 37, Application US/10096246A
Patent No. 6818748
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fulton, R. Elaine
APPLICANT: Alvi, Achar Z.
TILLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of TILLE OF INVENTION: Of TITLE OF INVENTION: Usus (VEE)
TITLE OF INVENTION: Usus (VEE)
TITLE OF INVENTION: Usus (VEE)
CURRENT APPLICATION NUMBER: US/10/096,246A
CURRENT APPLICATION NUMBER: US/10/096,246A
CURRENT FILING DATE: 2002-03-13
SOFTWARE: PatentIn Version 3.2
SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 650114
GENERAL INFORMATION:
APPLICANT: The Minister of National Defence, Government of Canada
APPLICANT: The Minister of National Defence, Government of Canada
APPLICANT: Fulton, R E
APPLICANT: Fulton, R E
APPLICANT: Nagata, Lesile
TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of MC
TITLE OF INVENTION: Scrv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
TITLE REFERENCE: NEL-0007
CURRENT APPLICATION NUMBER: US/10/092,246
CURRENT APPLICATION NUMBER: US/10/092,246
CURRENT PILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 36
TEMPORTH: APPLICATION OF SEQ ID NOS: 37
181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
                                                178 LLIFWSSTRHTGVPDRFTGSGSGTDFTLTISNAQSEDLADYFCHOYSSYPFTFGSGTKLE 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LENGTH: 240
; TYPE: PRT
CRGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-36
                                                                                                                                                      241 IKR 243
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US-10-096-246A-37
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                               181 LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: ANTI-EGFR SINGLE-CHAIN FUS AND ANTI-EGFR NUMBER OF SEQUENCES: 30 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 244;
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66.9%; Pred. No. 2.5e-65;
ive 27; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: MILLEN, WHITE, ZELANO & BRANIGAN, P.C.
STREET: 2200 CLARENDON BLVD. SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,497A
FILING DATE: 17-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 17-NOV-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/EP95/00978
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94104160.0
FILING DATE: 17-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94118970.6
FILING DATE: 02-DEC-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                               Sequence 20, Application US/08553497A Patent No. 5844093
                                                                                                                                                                                                                                                                                                                                APPLICANT: KETTLEBOROUGH, C. A. A. APPLICANT: BENDIG, MARY M. AAPPLICANT: ANSELL, KETTH H. AAPPLICANT: GUSSOW, DETLER
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ANSELL, KEITH H.
APPLICANT: GUSSOW, DETLEF
APPLICANT: ADAN, JAUNE
APPLICANT: MITJANS, FRANSESC
APPLICANT: ROSELL, ELISABET
APPLICANT: BLASCO, FRANCESC
APPLICANT: PIULATS, JAUNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: HAMLET-KING, DIANA
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: MEI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-243-6333
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Best Local Similarity 66.94
Matches 164; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acid
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APPLICANT: Alvi, Azhar E
APPLICANT: Nagata, Lealie
TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of MC
TITLE OF INVENTION: ScFV Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
FILE REPERENCE: NEL-007
CURRENT APPLICATION NUMBER: US/10/092,246
CURRENT FILING DATE: 2002-03-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 VKLIYYTSNLHSEVPSRFSGSGSGTDYSLTISNLEQEDIATYFCQQDFTLPFTFGGGTK 261
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Patent No. 6501314
GENERAL INFORMATION:
APPLICANT: The Minister of National Defence, Government of Canada APPLICANT: Fulton, R E
                                                                                                                                                                                                                                           Query Match 65.2%; Score 833.5; DB 2; Length 273; Best Local Similarity 67.2%; Pred. No. 1.2e-65; Matches 164; Conservative 26; Mismatches 51; Indels 3;
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US-10-092-246-37
; INPORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS: LENGTH: 273 amir.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin version 3.1
SEQ ID NO 37
LENGTH: 240
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                                                                                                                                                        TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-403-853-18
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Best Local Similarity
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Sequence 28, Appli Sequence 5, Appli Sequence 2, Appli Sequence 46, Appl

Sequence Sequence

Sequence 18, Ay Sequence 18, 1 Sequence 18, 1

Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 18, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 36, Appli Sequence 36, Appli Sequence 1635, Appli Sequence 1635, Appli Sequence 1635, Appli Sequence 1635, Appli Sequence 20, Appli

Sequence 1104, Ap Sequence 1104, Ap Sequence 40, Appl

Sequence 95,

Perfect score:

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Sequence:

Scoring table:

Searched:

Database

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5T4 scFv, designated
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US-10-496-179-2

US-10-496-179-3

US-10-496-179-3

US-10-496-179-5

US-10-496-179-5

US-10-496-179-5

US-10-496-179-5

US-10-496-179-5

US-10-496-179-5

US-10-14-716A-46

US-10-14-716A-46

US-10-27-66-18

US-10-27-64-35

US-10-96-246-35

US-10-96-246-35

US-10-96-246-37

US-10-96-246-37

US-10-96-246-37

US-10-96-246-37

US-10-99-246-114

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US-10-99-246-114

US-10-99-246-114

US-10-98-246-37

US-10-98-246-37

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US-10-39-34-11104

US-10-38-34-18-1104

US-10-138-56-40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kingsman, Alan
APPLICANT: Kingsman, Alan
APPLICANT: Bebbington, Christopher
APPLICANT: Barroll, Miles
APPLICANT: Bllard, Fiona
APPLICANT: Bllard, Fiona
APPLICANT: Kingsman, Susan
APPLICANT: Kingsman, Susan
APPLICANT: Myers, Kevin
APPLICANT: Lankandra, Abigail
TITLE OF INVENTION: VECTOR SYSTEM
FILE REFERENCE: 5326200020
CURRENT APPLICATION NUMBER: US/10/334,235
CURRENT APPLICATION NUMBER: US/10/60,585
PRIOR APPLICATION NUMBER: PCT/GB00/04317
PRIOR FILING DATE: 2000-11-13
PRIOR FILING DATE: 2000-11-13
PRIOR FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 40
SOFTWARE: PSESEE FOR WINDOWS Version 4.0
SSOFTWARE: PSESEE FOR WINDOWS VERSION 4.0
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APPLICANT: Oxfard Biomedica (UK) Ltd.
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| Cgn2_6/ptodata1/lpubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/lpubpaa/US06_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/lpubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/lpubpaa/US07_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/lpubpaa/US08_PUBCOMB.ppp:*
| Cgn2_6/ptodata1/lpubpaa/US08_PUBCOMB.ppp:*
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| Cgn2_6/ptodata1/lpubpaa/US09_NEW_PUB.ppp:*
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| Cgn2_6/ptodata1/lpubpaa/US09_NEW_PUB.ppp:*
| Cgn2_6/ptodata1/lpubpaa/US10B_PUBCOMB.ppp:*
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US-10-879-994-10
US-09-900-766-1
US-10-296-085A-19
US-10-296-085A-20
US-10-296-085A-27
US-10-296-085A-17
US-10-296-085A-17
US-10-296-085A-17
US-10-296-085A-17
US-10-296-085A-18
US-10-296-085A-18
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Maximum Match 100%
Listing first 45 summaries
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and is derived by analysis of
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Maximum DB seq length: 2000000000
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100.0%; Pred. No. 5.5e-89;
iive 0; Mismatches 0;
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APPLICANT: Bebbington, Christopher
APPLICANT: Bebbington, Christopher
APPLICANT: Bebbington, Christopher
APPLICANT: Elazd, Fiona
APPLICANT: Kingsman, Susan
APPLICANT: Kingsman, Susan
APPLICANT: Myers, Kevin
APPLICANT: Myers, Kevin
TITLE OF INVENTION: VECTOR SYSTEM
TITLE OF INVENTION: VECTOR SYSTEM
TITLE OF INVENTION: 2002-12-30
CURRENT APPLICATION NUMBER: US/10/334,235
CURRENT FILING DATE: 2002-10-29
PRIOR PLING DATE: 2000-11-29
PRIOR FILING DATE: 2000-11-39
PRIOR FILING DATE: 2000-11-13
PRIOR FILING DATE: 2000-11-13
NUMBER OF SEQ ID NOS: 40
SEQ ID NOS: 40
SECTUMARE: FastSEQ for Windows Version 4.0
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; OTHER INFORMATION: peptide of B7-1.5T4.1
US-10-334-235-39
                                                                                                                                                                                                                                                                             APPLICANT: Oxfard Biomedica (UK) Ltd. APPLICANT: Kingsman Alan
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Publication No. US20040131591A1
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APPLICANT: Stancopoulos, George D.
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Best Local Similarity 100.0
Matches 242; Conservative
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                                             1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY
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100.0%; Pred. No. 2.9e-89;
tive 0; Mismatches 0;
Mismatches
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US-10-334-235-38
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Publication No. US20040131591A1
PERERAL INFORMATION:
APPLICANT: Oxfard Biomedica (UK) Ltd.
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ORGANISM: Artificial Sequence
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Matches 243; Conservative
  243; Conservative
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LENGTH: 600
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GENERAL INFORMATION:

Sequence 169, Application US/10059261

Sequence 169, Application No. US200300778261

Publication No. US200300778261

SEQUENCE INFORMATION:

APPLICANT: BDELMAN, LENA

APPLICANT: BDELMAN, LENA

APPLICANT: BUNENTION: CHIMERIC MOLECULES CONTAINING A MODULE ABLE TO TARGET

TITLE OF INVENTION: FUNCTION OF THE PERMEABILITY TRANSITION PORE COMPLEX

TITLE OF INVENTION: (PTPC)

TITLE OF INVENTION: (PTPC)

FILE REFERENCE: 03495.0216

CURRENT APPLICATION NUMBER: US/10/059,261

CURRENT FILING DATE: 2002-08-29

PRIOR FILING DATE: 2001-02-02

NUMBER OF SEQ ID NOS: 325

SEQ ID NO 169

LENGTH: 331
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** OTHER INFORMATION: Description of Artificial Sequence: vector pACgp67-ScFv350

** OTHER INFORMATION: peptide sequence
US-10-059-261-169
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                                                                                                                                                                                                     181 LYTLSSSVTVPSSTWPSETVTCNVAHPASSTKVDKKIVPRDSGGPSEKSEEINEKDLRKK 240
                                                                                                                                                                                                                                                                                                                         241 SELQGTALGNLKQIYYYNSKAITSSEKSADQFLTNTLLFKGFFTGHPWYNDLLVDLGSTA 300
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                                                                                                                                                           121 AKTTPPSVYPLAPGSAAQTNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTFPAVLQSD 180
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  1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSPGKGLEWIGRINPNNGVTLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 LAVYFCQQDYNSPPTFGGGTKLEIKR 243
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ORGANISM: Artificial Sequence
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APPLICANT: Karow, Margaret
APPLICANT: Smith, Enic
TITLE OF INVENTION: HIGH AFFINITY FUSION PROTEINS AND THERAPEUTIC AND DIAGNOSTIC METH
TITLE OF INVENTION: USE
FILE REPERENCE: REG 203E2
CURRENT APPLICATION NUMBER: US/10/879,994
CURRENT APPLICATION NUMBER: 10/610,452
PRIOR FILING DATE: 2003-06-30
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 243
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Publication No. US20030039655A1
Publication No. US20030039655A1
APPLICANT: PORSBERG, GORAN
APPLICANT: ARTONSSON, EVA
APPLICANT: MALSE, BJORN
TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
FILE REFERENCE: P02188US0;10104199
CURRENT APPLICATION NUMBER: US/09/900,766
CURRENT FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                  Length 243;
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78.7%; Pred. No. 5.7e-68;
tive 19; Mismatches 31;
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LOCATION: (1)..(672)
CTHEN INFORMATION: Conjugate protein
US-09-900-766-1
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Best Local Similarity 78.7%
Matches 192; Conservative
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Best Local Similarity
Matches 227; Conserva
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TYPE: PRT
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119 SSGGGGGGGGGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQS 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179 PILLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTK 238
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                                        635 SSGGGGGGGGGGGGDIQMTQTTSSLSASLGDRVTISCRASQDIRNYLNWYQQKPDGT
                                                                                                                   179 PTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTK
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US-10-296-085A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MARY ELLEN DIGAN
TITLE OF INVENTION: IMMUNOTOXIN FUSION PROTEINS AND MEANS
TITLE OF INVENTION: FOR EXPRESSION THEREOF
FILE REFERENCE: 14028.0294U2
CURRENT APPLICATION NUMBER: US/10/296,085A
CURRENT FILING DATE: 2002-11-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
68.7%; Score 879; DB 16;
Best Local Similarity 70.1%; Pred. No. 1.3e-58;
Matches 171; Conservative 25; Mismatches 46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT FILLING DATE: A002-11-18
PRIOR APPLICATION NUMBER: 09/573,797
PRIOR FILING DATE: 2000-05-18
PRIOR PILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR PILING DATE: 1999-09-03
PRIOR PILING DATE: 1999-09-03
PRIOR PILING DATE: 1998-09-03
PRIOR PILING DATE: 1998-09-03
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PRIOR PILING DATE: 1996-10-29
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Publication No. US20040127682A1
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JONATHAN MARK HEXHAM
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ORGANISM: Artificial Sequence
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APPLICANT: JERRY T. THOMPSON
APPLICANT: JUNG-HEE WOO
APPLICANT: HUAIZHONG HU
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                                                                                                          146 NOEFKDKATLTADKSSNTAYMHLSSLTYEDSAVYYCARAAQATTF--DYWGQGTTLTVSS 203
                                                                                                                                                                 GGGGSGGGGGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
                                                                                                                                                                                                                                                                              LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
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APPLICANT: SHENGLIN MA
APPLICANT: JONATHAN MARK HEXHAM
TITLE OF INVENTION: IMMUNOTOXIN FUSION PROTEINS AND MEANS
TITLE OF INVENTION: FOR EXPRESSION THEREOF
FILE REFERENCE: 14028.029402
CURRENT APPLICATION NUMBER: US/10/296,085A
PRICATION NUMBER: US/10/296,085A
PRICATION NUMBER: US/10/296,085A
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US-10-296-085A-19
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PRIOR PILLAW DATE: 2006-05-18
PRIOR APPLICATION NUMBER: 09/380,484
PRIOR APPLICATION NUMBER: 09/380,484
PRIOR PLING DATE: 1999-09-03
PRIOR PLING DATE: 1999-09-03
PRIOR PLING DATE: 1999-03-03
PRIOR APPLICATION NUMBER: PCT/US98/04303
PRIOR APPLICATION NUMBER: PCT/US98/04303
PRIOR PLING DATE: 1996-10-29
PRIOR PLING DATE: 1997-10-29
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SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: JERRY T. THOMPSON
APPLICANT: JUNG-HEE WOO
APPLICANT: HUAIZHONG HU
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IKR 326
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61 NOKFKDKAILIVDKSSTTAYMELRSLTSEDSAVYYCARSTMI--TNYVMDYWGQVTSVTV 118
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APPLICANT: DAVID M. NEVILLE
APPLICANT: DANID M. NEVILLE
APPLICANT: JUNG-HEE WOO
APPLICANT: JUNG-HEE WOO
APPLICANT: SHENGLIN MA
APPLICANT: JUNATHAN MARK HEXHAM
APPLICANT: JUNATHAN MARK HEXHAM
APPLICANT: JUNATHAN MARK HEXHAM
APPLICANT: MARY ELLEN DIGAN
TITLE OF INVENTION: IMMUNOTOXIN FUSION PROTEINS AND MEANS
TITLE OF INVENTION: IMMUNOTOXIN THEREOF
FILE REFERENCE: 14028.0294U2
CURRENT APPLICATION NUMBER: US/10/296,085A
CURRENT FILING DATE: 2002-11-18
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                                                          Sequence 4, Application US/10496179; Sequence 4, Application No. US20050033034A1; GENERAL INFORMATION:
APPLICANT: Wowartie AG APPLICANT: Bngel, Guenter:
TITLE OF INVENTION: New combination; FILE REFREENCE: TY4.32202A; CURRENT APPLICATION NUMBER: US/10/496,179; CURRENT FILING DATE: 2004-05-20; PRIOR PRIOR FILING DATE: 2001-11-28; PRIOR PRINCATION NUMBER: GB 0128509.7; PRIOR PRINCATION NUMBER: GB 0128509.7; PRIOR PRINCATION NUMBER: GB 0128509.7; PRIOR PRINCATION NUMBER: GB 0128510.5; PRIOR FILING DATE: 2001-11-28
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PRIOR FILING DATE: 2000-05-18
PRIOR APPLICATION NUMBER: 09/380,484
                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 895
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Best Local Similarity 70.1
Matches 171; Conservative
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US-10-296-085A-17
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APPLICANT: SHENGLIN MARK HEXHAM
APPLICANT: JONATHAN MARK HEXHAM
APPLICANT: JONATHAN MARK HEXHAM
APPLICANT: JONATHAN MARK HEXHAM
TITLE OF INVENTION: FOR EXPRESSION THEREOF
FILE REPERENCE: 14028 0.29402
CURRENT APPLICATION NUMBER: 09/573,797
PRIOR APPLICATION NUMBER: 09/573,797
PRIOR APPLICATION NUMBER: 09/380,484
PRIOR FILING DATE: 1999-09-03
PRIOR PILING DATE: 1999-03-05
PRIOR PILING DATE: 1996-03-05
PRIOR PILING DATE: 1996-03-05
PRIOR PILING DATE: 1996-03-05
PRIOR PILING DATE: 1999-03-05
PRIOR PILING DATE: 1999-03-05
PRIOR PILING DATE: 1999-03-05
PRIOR PILING DATE: 1999-03-05
PRIOR PILING DATE: 1999-10-30
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US-10-296-085A-27
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Publication No. US20040127682A1
GENERAL INFORMATION:
APPLICANT: DAVID M. NEVILLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
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JUNG-HEE WOO
HUAIZHONG HU
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Matches 171; Conservative
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SOFTWARE: FastSEQ for Win
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LENGTH: 895
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Best Local Similarity 70.1
Matches 171; Conservative
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APPLICANT: HUAIZHONG HU
APPLICANT: HUAIZHONG HU
APPLICANT: SHENGLIN MA
APPLICANT: JONATHAN MARK HEXHAM
APPLICANT: JONATHAN MARK HEXHAM
TITLE OF INVENTION: INMUNOTOXIN FUSION PROTEINS AND MEANS
TITLE OF INVENTION: INMUNOTOXIN FUSION PROTEINS
TITLE OF INVENTION: POR EXPRESSION THEREOF
FILE REFERENCE: 14028.029402
CURRENT APPLICATION NUMBER: US/10/296,085A
CURRENT APPLICATION NUMBER: 09/573,797
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-03
PRIOR FILING DATE: 1999-09-05
PRIOR FILING DATE: 1999-03-05
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US-10-296-085A-17
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PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 09/389,565
PRIOR PILING DATE: 1999-09-03
PRIOR PELING DATE: 1998-03-03
PRIOR APPLICATION NUMBER: PCT/US98/04303
PRIOR APPLICATION NUMBER: 08/739,703
PRIOR PILING DATE: 1996-10-29
PRIOR FILING DATE: 1996-10-29
PRIOR FILING DATE: 1997-03-05
PRIOR PELING DATE: 1997-03-05
PRIOR FILING DATE: 1997-03-05
NUMBER OF SEQ ID NOS: 122
SOFFWARE: FASTSEQ FOR WINDOWS Version 4.0
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Publication No. US20040127682A1
GENERAL INFORMATION:
APPLICANT: DAVID M. NEVILLE
APPLICANT: JERRY T. THOMPSON
APPLICANT: JUNG-HEE WOO
APPLICANT: HUNG-HEE WOO
                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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Matches 171; Conservative
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US-10-296-085A-18
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LENGTH: 896
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSGGGGSGGGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQS
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                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial Sequence FEATURE: OCHER INFORMATION: Description of Artificial Sequence:/Note OTHER INFORMATION: synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: SHENGLIN MA
APPLICANT: JONATHAN MARK HEXHAM
APPLICANT: JONATHAN MARK HEXHAM
APPLICANT: MARY ELLEN DIGAN
TITLE OF INVENTION: IMMUNOTOXIN FUSION PROTEINS AND MEANS
TITLE OF INVENTION: FOR EXPRESSION THEREOF
CURRENT APPLICANTON NUMBER: US/10/296,085A
CURRENT FILING DATE: 2002-11-18
PRIOR FILING DATE: 1996-10-29
PRIOR APPLICATION NUMBER: 60/039,987
PRIOR FILING DATE: 1997-03-05
PRIOR APPLICATION NUMBER: 60/008,104
PRIOR FILING DATE: 1995-10-30
NUMBER OF SEQ ID NOS: 122
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 896
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PRIOR PILING DATE: 2000-05-18
PRIOR PLILING DATE: 2000-05-18
PRIOR PLILING DATE: 1999-09-03
PRIOR PLILING DATE: 1999-09-03
PRIOR PLILING DATE: 1999-09-03
PRIOR PLILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: PCT/US98/04303
PRIOR APPLICATION NUMBER: PCT/US98/04303
PRIOR PLILING DATE: 1998-03-05
PRIOR PLILING DATE: 1996-10-29
PRIOR PLILING DATE: 1997-03-05
PRIOR PLILING DATE: 1997-03-05
PRIOR PLILING DATE: 1997-03-05
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PRIOR FILING DATE: 1997-03-05
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Publication Wo. US20040127682A1
GENERAL INFORMATION:
APPLICANT: DAVID M. NEVILLE
APPLICANT: JUNG-HEE WOO
APPLICANT: JUNG-HEE WOO
APPLICANT: HUAIZHONG HU
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NUMBER OF SEQ ID NOS: 122
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61 NOKFKDKAILIVDKSSTTAYMELRSLTSEDSAVYYCARSTMI--TNYVMDYWGQVTSVTV 118
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                                                                                            179 PILLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCOODYNSPPTFGGGTK 238
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                                                                                                                                                                                                                                                                                                Sequence 3, Application US/10496179
| Publication No. US20050033034A1
| GENERAL INFORMATION:
| APPLICANT: Novartis AG
| APPLICANT: Engel, Guenter
| TILE OF INVENTION: New combination
| FILE REFERENCE: TX/4-32202A
| CURRENT FILING DATE: 2004-05-20
| PRIOR APPLICATION NUMBER: US/10/496,179
| PRIOR APPLICATION NUMBER: GB 0128509.7
| PRIOR FILING DATE: 2001-11-28
| PRIOR FILING DATE: 2001-11-28
| PRIOR FILING DATE: 2001-11-28
| NUMBER OF SEQ ID NOS: 7
| SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)..(896)
; OTHER INFORMATION: synthetic construct US-10-496-179-3
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Matches 171; Conservative
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ORGANISM: Artificial
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NAME/KEY: PEPTIDE
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US-10-496-179-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          516 EVQLQQSGPELVKPGASMKISCKASGYSFTGYTMMWVKQSHGKNLEWMGLINPYKGVSTY 575
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                                                                                                  ) OTHER INFORMATION: Description of Artificial Sequence:/Note; OTHER INFORMATION: synthetic construct
US-10-296-085A-26
                                                                                                                                                                                        Query Match 68.7%; Score 879; DB 16; Length 8 Best Local Similarity 70.1%; Pred. No. 1.3e-58; Matches 171; Conservative 25; Mismatches 46; Indels
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70.1%; Pred. No. 1.38-58;
ive 25; Mismatches 46; Indels
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Publication No. US20050033034A1
GENERAL INFORMATION
APPLICANT: NOTE:
TITLE OF INVENTION: New combination
FILE REFRENCE: TX/4-32202A
CURRENT APPLICATION NUMBER: US/10/496,179
CURRENT FILING DATE: 2004-05-20
PRIOR APPLICATION NUMBER: US 0128509.7
PRIOR PILING DATE: 2001-11-28
PRIOR FILING DATE: 2001-11-28
PRIOR FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 7
SEQ ID NO 2
SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 26 LENGTH: 896
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CTHER INFORMATION: synthetic construct
US-10-496-179-2
                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 70.1<sup>3</sup>
Matches 171; Conservative
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ORGANISM: Artificial
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NAME/KEY: PEPTIDE
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575

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GenCore version 5.1.6 (Copyright (c) 1993 - 2005 Compugen Ltd.
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OM protein - protein search, using sw model

March 11, 2005, 14:49:22 ; Search time 16 Seconds (without alignments) 1461.292 Million cell updates/sec Run on:

US-10-016-686-1 1279 1 EVQLQQSGPDLVKPGASVKI......QQDYNSPPTFGGGTKLEIKR 243 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES & Query Result

	Description	Ig heavy chain V r	ingle chain	specific	neavy chai	neavy	neavy	neavy chain	kappa chain	neavy chain	neavy chain pr	neavy chain	neavy	heavy chain	Ig heavy chain (my	neavy chain	neavy chain V	heavy chain	heavy chain V-	neavy	heavy chain	neavy	heavy	heavy	neavy	neavy	Ig heavy chain V r	anti-glycoprotein	Ig kappa chain pre	anti-glycoprotein
	ID	A56446	S41374	JC5322	A49982	137267	PS0057	A27609	S37484	C37267	PL0011	B30502	826319	MHMS4E	T01407	MHMSJS	MHMS38	PH0100	809957	E37267	H32513	PH0887	F30502	A37267	B53285	826320	855535	F45722	S04577	E45722
	g ;	~	~	~	~	7	~	~	~	7	7	~	~	-	~		-	~	~	~	~	~	N	~	~	N	~	N	~	0
	Match Length		249	233	120	128	135	139	225	128	151	144	114	117	140	117	118	125	112	122	137	122	119	128				120	127	120
Kner y	Match	57.2	55.5	50.5		39.5	39.5	38.9	38.8	38.6	37.8	37.6	37.6	37.6	37.6	37.5	37.5	37.4	37.4	37.2	37.2	37.1	37.1	36.9	36.9		36.4	36.4	36.4	36.3
	Score	3	710	646	516	502	501	498	496.5	494	483.5	481.5	481	480.5	480.5	479.5	479	478.5	478	476	476	475	474	472	471.5	471	465	465	465	464
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A341374

Single chain Fv antibody - mouse

Single chain Fv antibody - mouse

Cipacise: Mus musculus (house mouse)

Cipacise: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

Cipacession: S41374

RiArtasenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.

Submitted to the EMBL Data Library, January 1994

A;Description: Construction and functional characterization of a single chain Fv antibod)

A;Reference number: S41374

RESULT 2

Ig heavy chain V r	neavy	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V r	Ig heavy chain V r	i-dig	Ig heavy chain V r	_	LB lead	Ig heavy chain V r	Ig gamma chain - m	датта-2а ср	Ig kappa chain V-J	chain	anti-DNA autoantib
F37266	PS0024	PH0974	PH0099	855534	S20639	PH0105	803305	S41394	PC4402	PN0444	838950	S40295	S09964	PH0975	PL0200
N	N	N	N	7	N	~	~	7	4	0	N	~	7	~	7
121	139	113	119	113	125	138	117	120	287	150	246	446	107	108	118
36.2	36.1	36.1	36.1	36.0	35.9	35.9	35.8	35.8	35.7	35.7	35.7	35.7	35.6	35.6	35.5
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463.5	462	461.5	461.5	460	459	459	458	4	4	4	4	4	4	4.	453.

ALIGNMENTS

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Best Local Si
Matches 99;
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A)Experimental source: hydricloma cell
C;Comment: This protein specifically binds the tumor suppressor protein p53. It restores
                                                                                                                                                                                                                                                                                                                                                                                                                                        61 VPRFQDKATITADISSNTAYLLLSSLTSEDTAVYYCARRDTLYTS--LGYWGQGSTVTVS 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p53.
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                                                                                                                                                                          Length 249;
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                                                                                                                                                                     Query Match
Best Local Similarity 56.6%; Pred. No. 1.3e-43;
Matches 141; Conservative 41; Mismatches 59;
                          A;Status: preliminary
A;Molecule type: DNA
Residues: 1-249 cART>
A;Cross-references: EMBL:229480
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239 AGTKLELKR 247
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A; Accession: S41374
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RESULT

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In heavy chain V region (129) - mouse C. Species: Mas musculus (house mouse)
C.Species: Mas musculus (house mouse)
C.Accession: 137267
B.R.Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Balol. Chem. 266, 660-76613, 1991
A.Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
A.Reference number: A38740; MUD:91177923; PMID:1706720
A.Accession: 137267
A.Status: preliminary; not compared with conceptual translation
A.Status: preliminary; not compared with conceptual translation
A.Status: I-128 < RUF>
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Superfamily: immunoglobulin homology < NWM>
Cispecies: Mus musculus (house mouse)
Cibate: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
Cibate: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
Cibate: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
Ribin, C.; Kieber-Emmons, T.; Villalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleyman, J. Biol. Chem. 269, 2805-2813, 1994
A;Title: Topology of an amiloride-binding protein.
A;Reference number: A49982; MulD:94132051; PMID:8300613
A;Reference number: A49982
A;Reference number: A49982
A;Reference number: A49982
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A;Residues: 1-120 <LIN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   th 40.3%; Score 516; DB 2; Similarity 82.5%; Pred. No. 3.6e-30; 99; Conservative 5; Mismatches 16
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Ig heavy chain V region (Py69) - mouse

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Ig heavy chain V region (Py69) - mouse

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A, Experimental source: cell line 4Cl1
C, Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylchol
C, Superfamily: immunoglobulin v region; immunoglobulin homology
C, Keywords: heterotetramer; immunoglobulin
F,1-19/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 GAHGSIVMTQTPKFLLLSAGDRVTITCKASQSVSNDVAWYQQKPGQSPKLLIYYASSRYT 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain precursor V region (4C11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C;Accession: PL0011
R;Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
MOI. Immunol. 25, 33-40, 198 stimulatory anti-idiotypic antibodies.
A;Title: Structural basis of stimulatory anti-idiotypic antibodies.
A;Reference number: PL0011; MUID:88142863; PMID:3125424
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-225 <DUC>
A;Cross-references: EMBL:X70424; NID:g406254; PIDN:CAA49869.1; PID:g406255
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Stywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  132 GGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPTLLISYTSSRYA
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Pred. No. 1.4e-28;
9; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                 38.8%; Score 496.5; DB 2; Length ilarity 87.5%; Pred. No. 1.8e-28; Conservative 3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 38.6%;
1 Similarity 77.2%;
95; Conservative
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                                                                                                                     A;Accession: PS0057
A;Molecule type: DNA
A;Molecule type: DNA
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A;Molecule type: DNA
C;Molecule                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biochem. 104, 337-343, 1988
A;Title: Biased expression of variable region gene families of the immunoglobulin heavy
A;Reference number: PS0057; MUID:89197817; PMID:2467902
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Ig kappa chain - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Species: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C;Accession: S37484
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EVQLQQSGPELVXPGASVKISCKASGYSFTGYFMMVKQSHGKSLEWIGRINPYNGDTFY
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A;Residues: 1-139 <KLE>
A;Cross-references: EMBL:M19401; NID:g195441; PIDN:AAA38303.1; PID:g553992
C;Genetics:
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F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-139/Product: Ig heavy chain V region 129 #status predicted <VAR>
F;34-117/Domain: immunoglobulin homology <IMM>
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Pred. No. 8.2e-29;
8; Mismatches 16; Indels
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82.5%; Pred. No. 4.8e-29;
iive 6; Mismatches 11;
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99; Conservative
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Matches 96; Conservative
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A;Accession: S37484
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Best Local Similarity

Matches

Query Match

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Ig heavy chain V region (MOPC 104E) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 30-Nov-1979 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
C;Accession: A02039
R;Kabry, M.R.; Fuhrman, J.S.; Schilling, J.W.; Rogers, J.; Sibley, C.H.; Hood, L.E.
B;Ochemistry 21, 5415-5424, 1982
A;Title: Complete amino acid sequence of a mouse mu chain: homology among heavy chain cor A;Reference number: A02039
A;Title: Complete amino acid sequence of a mouse mu chain: homology among heavy chain A;Reference number: A2039
A;Molecule type: protein
A;Reference number: ACKBP-
A;Coession: A12039
A;Molecule type: protein
A;Residues: 1-117 *KKBP-
A;Coess-references: UNIPROT:P01756
C;Comment: The glycosylated asparagine residue does not have the usual N-X-S/T context ar C;Comment: The glycosylated asparagine; immunoglobulin homology
C;Reywords: glycoprotein; heterotetramer; immunoglobulin
F;15-594/Domain: immunoglobulin homology cIMM>
F;12-96/Disulfide bonds: #status predicted
F;55/Binding site: carbohydrate (ARN) (rowslant)
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Igheavy chain (myeloma M104E) - mouse (fragment)

C;Species: Mus sp. (mouse)

C;Species: Mus sp. (mouse)

C;Accession: T01407

R;Takhashi, S.; Matsuura, Y.; Taniguchi, T.; Tamura, H.; Bitch, S.; Onishi, S.; Yamamotc

Microbiol. Immunol. 36, 855-863, 1992

Microbiol. Immunol. 36, 855-863, 1992

Myrtle: Molecular analysis of immunoglobulin heavy chain genes coding for idiotypic and A;Reference number: Z14317; MUID:93116638; PMID:1474935

A;Reference number: MUID:93116638; PMID:1474935

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-140

A;Molecule type: mRNA

A;Residues: TARA

A;Residues: TARA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 KDKAILITVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNY--VMDYWGQVTSVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 KGKATLITVDKSSSTAHMELLSLTSEDSAVYYCGKD----GYYGAMDYWGQGTSVTVSS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 QQSGPELVKPGASVKISCKASGYSFTGYFMNWVKQSHGKSLEWIGRINPYNGDIFYNQKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 QQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLYNQKF
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                        C; Superfamily: immunoglobulin V region; immunoglobulin homology
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                 11; Indels
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                                                                                                                                                                                                                                                37.6%; Score 481; DB 2;
80.5%; Pred. No. 1.1e-27;
tive 6; Mismatches 11.
                                                                         C; Keywords: heterotetramer; immunoglobulin F;11-94/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                           95; Conservative
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Best Local Similarity 78.3
Matches 94; Conservative
                                                                                                                                                                                                                                                                                                             Best Local Similarity
Matches 95; Conserva
                                                                                                                                                                                                                                                                  Query Match
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256319
19 Abayy chain V region - mouse (fragment)
19 Gispecies: Mus musculus (house mouse)
CiSpecies: Mus musculus (house mouse)
CiSpecies: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 21-Jan-2000
CiAccession: 826319
R.Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A.Title: Antibodies that are specific for a single amino acid interchange in a protein A.Reference number: 826309; MUID:91341421; PMID:1908510
A.Accession: 826319
A.Accession: S2319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
F;20-136/Product: Ig heavy chain V region 4C11 "#status predicted <MAT> F;34-117/Domain: immunoglobulin homology <IMM> F;50-47/Region: complementarity-determining 1 F;60-85/Region: complementarity-determining 2 F;118-125/Region: complementarity-determining 2 F;118-125/Region: Complementarity-determining 3 F;137-151/Domain: C region (fragment) #status predicted <COR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
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                                                                                                                                                                                                                                                                                                                                                                                                                            37.8%; Score 483.5; DB 2; Length 151; 78.0%; Pred. No. 9.6e-28; ive 7; Mismatches 11; Indels 9
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A;Molecule type: mRNA A;Residues: 1-144 <EIL>

Query Match

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A;Status: preliminary

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RESULT 15
MHMSJ5
Ig heavy chain V region (J558) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: A26242
R;Schilling, J; Clevinger, B; Davie, J.M.; Hood, L.
Nature 283, 35-40, 1980
A;Title: Amino acid sequence of homogeneous antibodies to dextran and DNA rearrangements
A;Reference number: A26242; MUID:80078170; PMID:6765983
A;Residues: 1-117 <SCHA
A;Molecule type: protein
A;Residues: 1-117 <SCHA
A;Molecule type: protein
A;Residues: UNIPROT:P01757
A;Note: the sequences of 10 hybridoma proteins that also bind dextran differ from that E
C;Comment: This protein binds dextran.
C;Comment: This protein binds dextran.
C;Comment: This protein binds dextran.
C;Comment: manunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; hybridoma; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
F;22-96/Disulfide bonds: #status predicted

3; 37.5%; Score 479.5; DB 1; Length 117; 78.3%; Pred. No. 1.4e-27; tive 7; Mismatches 16; Indels 3; Query Match
Best Local Similarity 78.3
Matches 94; Conservative

61 NOKPKDKAILITVDKSSTTAYMELRSLISEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120 9 9 1 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSHGKSLEWIGDINPNNGGTSY 1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY Gaps

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Search completed: March 11, 2005, 14:56:09 Job time : 23 secs

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                                                                                                                                                                                                                                                                                                                        STRAIN=Balb/C;
MEDLINE=2285326; PubMed=12860977; DOI=10.1074/jbc.M306877200;
MEDLINE=2285326; PubMed=12860977; DOI=10.1074/jbc.M306877200;
Peter J.C., Effekhari P., Billiald P., Wallukat G., Hoebeke J.;
serve single chain antibody variable fragment as inverse agonist for the beta-2 adrenergic receptor.";
J. Balol. Chem. 278:36740-36747(2003).
BMBL; AJ574851; CAE00495.1; -.
HSSP; POI751; 1A6W.
InterPro; IPR007110; Ig-like.
InterPro; IPR007110; Ig-like.
InterPro; IPR00396; Ig-v.
SMART; SM00406; IGV; 2.
PROSITE; PS50835; IG_LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY
                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64.8%; Score 828.5; DB 2; Length 243; llarity 66.1%; Pred. No. 4.1e-58; Conservative 30; Mismatches 47; Indels 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                  243 AA; 25976 MW; BEFFF64D2DCF4F76 CRC64;
                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                   243 AA
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Q8K172
HV07_MOUSE
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0924R3
0924R6
0920E8
092404
092404
0924R7
                                                                                                                                                                                                   PRT;
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01-OCT-2003 (TrEMBLrel. 25, C;
01-OCT-2003 (TrEMBLrel. 25, L;
01-MAR-2004 (TrEMBLrel. 26, L;
SCFV 6H8 procein (Fragment).
 00000000000000
                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
ses 160; Conserv
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
NCBI_TaxID=10090;
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Query Match.
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Q6kb05 1
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0926xe9
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0926xe0
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         version 5.1.6
- 2005 Compugen Ltd.
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Q6KB05
Q6KB05
Q6SZC8
Q92YR0
Q92YR0
Q92ES1
Q92KB9
Q92ES2
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Maximum Match 100%
Listing first 45 summaries
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         GenCore (c) 1993
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           118 TVSSGGGGGGGGGGGGGDIVMAQSPSSLSVSAGEKVIMSCKSSQSLLNSRNQKNYLAW 177
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I antibody secreted from myeloma cells.";
I m. Antibodies Hybridomas 6:161-166(1995).

EMBL; S82433; AAB37424.2; -...

EMBL; S82433; AAB37424.2; -...

IR InterPro; IPR003599; IG.:

IR InterPro; IPR003599; Ig.cl.:

IR InterPro; IPR003596; Ig.cl.:

IR InterPro; IPR003596; Ig.cl.:

IR InterPro; IPR003596; Ig.cl.:

IR InterPro; IPR003596; Ig.cl.:

IR InterPro; IPR003596; Ig.cl.:

IR Ffam; PR00470; IG.:

IR SMART; SM00409; IG; 3.

SMART; SM00409; IG; 3.

SMART; SM00406; IGC2; 2.

REARRY; SM00406; IGC2; 2.

REARRY; SM00406; IGV; 2.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TAXID=10095;
                                                                                                                                                                                                                                                                                                                                                            Query Match 58.9%; Score 753.5; DB 2; Length 255; Best Local Similarity 57.9%; Pred. No. 4.1e-52; Matches 146; Conservative 37; Mismatches 56; Indels 13.
G., Tugler J., Maurice D., Roegel J.C.,
             Eriand J.P., Hobbeke J.; Salt J. Briand J.P., Hobbeke J.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. EMBL; AJ746180; CAG34081.1; -. HSSP; P01837; IRCR. InterPro; IPR003599; Ig. InterPro; IPR00710; Ig-1ike. InterPro; IPR00710; Ig-2. SMART; SM00409; IG; 2. SMART; SM00406; IGv; 2. FROSITE; PS50835; IG_LIKE; 2. NON TER I. I. T. SEQÜENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 SGGGGSGGGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSP 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 61.0%; Score 780.5; DB 2; Length 244; Best Local Similarity 61.5%; Pred. No. 2.7e-54; Matches 150; Conservative 35; Mismatches 58; Indels 1.
                                                                                                                                                                                                                                                                                                                                                       244 AA; 26127 MW; 4B1F17868338F2BF CRC64;
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                     Last sequence update)
Last annotation update)
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Name=scFv B8E5;
                                                                                       0652C8,
25-OCT-2004 (TYENBLYEL 28,
25-OCT-2004 (TYENBLYEL 28,
25-OCT-2004 (TYENBLYEL 28,
Single-chain Fv (Fragment).
                                                                      PRELIMINARY;
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                                                                                                                                                                                                                                                       Homo sapiens (Human)
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238
                                        218 LLVYNAKTLADGVPSRFSGSGSGTQYSLKINSLQPEDFGSYXCQHFWTTPYTFGGGTKLE 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGGGSGGGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDILINE=9110165; PubMed=9509426;

A Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,

Yi K.S., Suh P.C., Ryu S.H., Chung H.K.;

Yi K.S., Suh P.C., Ryu S.H., Chung H.K.;

"Cloning and characteriation of englance of constant of a single-chain FV molecule (scFV).";

monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and generation of a single-chain FV molecule (scFV).";

MOI. Cells 7:816-819 (1997).

REMBL; 018667; AAB48044.1; -..

RP PIR; 519967; 519967.

RP PIR; 519967; 519967.

RP PIR; 519967; 519967.

RP PIR; 519679; 519967.

RP PIR; 5199679; 519967.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 QVKLÓQSGPELKKÞGETVKISCKASGYTFTDYGMNWVKQAPGKGLKWMGWINTYTGEPTY
                     LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EVOLOQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY
                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 241;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241
26086 MW; 0276887248E9C771 CRC64;
                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54.8%; Score 701.5; DB 2;
54.3%; Pred. No. 5.3e-48;
ive 47; Mismatches 58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                240 AA.
                                                                                                                                                                                                                                                  241 AA
                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequenc
01-MAR-2004 (TrEMBLrel. 26, Last annotat
Anti-CEA 79 single chain Fv (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q65ZC9 PRELIMINARY; PRT; Q65ZC9; (TrEMBLrel. 28, Created)
                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 54.3
Matches 133; Conservative
                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
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241 AA;
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                                                                                                      241 IKR 243
                                                                                                                                             278 IKR 280
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SEQUENCE
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                                                                                                                                                                                                                               61 NQKFKDKAILITVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
                                                                                                                                                                                                                                                    80 NEKFKGKATLTADKSSSTAYMQLNSLTSEDSAVYFCKRS-----YYGHWGQGTTLT-GS 132
                                                                                                                                                                                                                                                                                                                GGGGSGGGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
                                                                                                                                                                                                                                                                                                                                     133 GGGSGGGGGGGGGSRIQMTQSPASLSVSVGELVTITCRASENIYSNLAWYQQKQGKSPQ 192
                                                                                                                                                                                                                                                                                                                                                                                             LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGGGTKLE 240
                                                                                                                                                                                                                                                                                                                                                                                                                     100 TPSLKDKFIISRDNAKNTLYLQMSKVRSEDTALYYCARASYYGHSA--YWGQGTTVTVSS 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGGSGGGGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSVSNDVAWYQQKPGQSPT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        158 GGGSGGGGGGGGGGDIELTQSPASLSASVGETVTITCRASGNIHNYLAWYQQXQGKSPQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                  20 QVQLQQSDAELVKPGASVKISCKASGYTFTDHAIHWAKQKPEQGLEWIGYISPGNDDIKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 QVKLQQSGGGLVKPGGSLKLSCAASGSDFSRYWNSWVRQAPGKGLEWIGEINPDSSTINY
                                                                                                                                             1 EVQLOQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY
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                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shinohara N., Demura T., Fukuda H.; "Isolation of a vascular cell wall-specific monoclonal antibody recognizing a cell polarity by using a phage display subtraction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                                              DB 2; Length 487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.9%; Score 702; DB 2; Length 298;
ilarity 54.3%; Pred. No. 6.2e-48;
Conservative 41; Mismatches 68; Indels
                                                       Query Match
Best Local Similarity 59.5%; Pred. No. 5.4e-51;
Matches 144; Conservative 37; Mismatches 54; Indels
PROSITE; PS00290; IG MHC; UNKNOWN 1.
SEQUENCE 487 AA; 53578 MW; C7BAB69F30555504 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSIȚE, PS50835, IG LIKE; 2.
SEQUENCE 298 AA; 31867 MW; B0F96B8A17004317 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000)
EMBL, AB036341, BAA88633.1; -.
PIR, A33933; A33933.
PIR, S19112; S19112.
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01-MAY-2000 (TrEMBLrel. 13, Last seque
01-OCT-2003 (TrEMBLrel. 25, Last annot
CN 8 single chain antibody.
Name=CN 8 scFv;
synthetic construct.
ocher sequences; artificial sequences.
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 2.
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InterPro; IRR07110; Ig-11ke.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR0045; Ig_v.
SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 2.
PROSITE; PSS0035; IG LIKE; 2.
                                                                                                                                                                                                                                                   Matches 128; Conservative
InterPro; IPR003599; Ig.
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                                                                                                                                                                                                                                    Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPFFGGGTKLE 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NOKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10095;
                                                                                                 Eukaryota, Metazona, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54.6%; Score 698.5; DB 2; Length 240; 56.0%; Pred. No. 9.2e-48; tive 36; Mismatches 68; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240 AA; 25569 MW; FDCFD3645F64B373 CRC64;
                                                                                                                                                                                                                                                        Kontermann R.E., Wing M.G., Winter G.,
"Complement recruitment using bispecific diabodies.";
Nat. Biotechnol. 15:629-631(1997).
  25-OCT-2004 (TrEMBLrel. 28, Last sequence update) 25-OCT-2004 (TrEMBLrel. 28, Last annotation update) Single-chain Fv (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                 STRAIN=C1q/7;
MEDLINE=97362799; PubMed=9219263;
                                                                                                                                                                                                                                                                                                                  EMBL, Y13056; CAA73499.1; -. Interpro; IPR003599; Ig. Interpro; IPR007110; Ig-like. Interpro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                             PERM; PF00047; 1g; 2.
SMART; SM00409; 1G; 2.
SMART; SM00406; 1G; 2.
PROSITE; PS50835; 1G LIKE; 2.
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 56.08
Matches 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                    Homo sapiens (Human)
                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=B3 (Fv) - PE40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238 IKR 240
                                                                                                                                                    NCBI_TaxID=9606;
                                                                     Name=scFv;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                            61 NOKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS
                                                                                                                                                                                                                                                                                                                                                                                                GGGGSGGGGTGGGGSSIVMTQTPTFLLVSAGDRVTITCKASQSV--SND---VAWYQQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         176 GQSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQAEDLAVYFCQQDYNSPPTFGG
                                                                                                                                                                                  1 EVOLOQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY
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the repair of intestinal epithelium after irradiation in mice.";
World J. Gastroenterol. 6:709-717(2000).
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Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
EMBL; AF240168; AAK43733.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                               Length 248;
                                                                                                                                 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; POLGES; 1QNZ.
SMART; SMO0406; IGV; 1.
PROSITE; PSSOB35; IG LIKE; 1.
NON TER 218 23013 MW; 527E4FA8F7982817 CRC64;
NON TER 248 248
SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              092551 PRELIMINARY; PRT; 218 AA. 092551; 01-DEC-2001 (TrEMBLrel. 19, Created) 01-DEC-2001 (TrEMBLrel. 19, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) MRP5 (Fragment).
                                                                            51.2%; Score 655; DB 2;
51.8%; Pred. No. 2.8e-44;
iive 45; Mismatches 68;
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MEDINE-22ECH II. TISSUE-Mammary tumor;

MEDINE-228CH II. TISSUE-Mammary tumor;

MEDINE-228825; PubMed-12477932; DOI=10.1073/pnas.242603899;

MEDINE-228825; PubMed-12477932; DOI=10.1073/pnas.242603899;

MALSTAINE-228REH II. Pelmodd E.A., Grouse L.H., Derge J.G.,

MALSTAINE-228REH II. Pelmodd E.A., Grouse L.H., Derge J.G.,

MALSTAINE S.F., Zeeberg B. Buercow K.H., Schaefer C.F., Bhat N.K.,

MALSTAINE S.F., John M. M., Perer M. M., Rubin G.M., Hong L.,

MA. Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheez T.E.,

MA. Stapleton M.J., Dedin T.B., Toshiyuki S., Carninci P., Prange C.,

MA., Peters G.J., Abramson R.D., Mullahy S.J.,

MARA S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

MARA S.S., Worden P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

MALIALON D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Milalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Milting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Makeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Makeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Makeeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

MARA S.J., Marra M.A.,

M. Green E.D., Dickson M.C.,

M. Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

M. Green E.D., Marra M.A.,

M. G
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                                                                                                                                                                                                                                                       Cui D., Zeng G., Yan X., Li X., Su C.; and continuated for sepairing of intestinal epithelium of the irradiated mice by treatment with the intestinal RNA of mice of
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                                                                                               "Mechanism of exogenous nucleic acids and their precursors improving
the repair of intestinal epithelium after irradiation in mice.";
World J. Gastroenterol. 6:709-717(2000).
                                                                                                                                                                                                                                                                                                                                         the same strain.";
Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
BEBL; AFS40167; AAK43732.1; -.
HSSP; PO1751; 1A6W.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                 Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.
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PROSITE; PSS0835; IG LIKE; 1.
SEQUENCE 170 AA; 17978 MW; S042823CC6C10F38 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein Al324046.
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STRAIN=BALB/C;
PubMed=11819679;
                                                                                                                                                                                                                                    STRAIN-BALB/C;
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Q7TMK1;
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                                                                                                                                                                                      63 AEEFKGRFAFSLETSASTAYLQISNLKNEDTATYFCMRWDYDGGFA--YWGGGTTVTVSS
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                                                                                 61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS
                                                      EVQLQQSGPDLVKPGASVKISCKASGYSFTGYYMHWVKQSHGKSLEWIGRINPNNGVTLY
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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     58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clemens A., Rademaekers A., Specht C., Koelsch E.; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases. EMBL, AJ225174; CA865237.1; -. HSSP; P115; F3392. HSSP; P01751; INQB. HSSP; P01751; INQB. HSSP; P01751; INQB. HSSP; P01751; INQB. HSSP; P01751; INQB. HSSP; P01751; INQB. HSSP; P01751; INQB. HSSP; P01751; INQB. HSSP; P01751; INQB. HSSP; IQ—V. SWART; SMO0406; IGV; I.
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                                                                                                                                                                                                                                                                                                                                                                    177 QSPTLLISYTSSRYAGVPDRFIGSGYGTDFTFTISTLQ 214
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  42; Mismatches
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(TrEMBLrel. 13, I
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     Matches 112; Conservative
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01-DEC-2001 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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SEQUENCE FROM N.A.
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Gaps

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Rueff-Juy D., Marche P.N., Dragol, T. Cazenave P.-A.;

"Unctional diversity of H and L chains allows the coexpression of two mutually exclusive idiotopes (Idilo4 and Idi558).";

"Unmunol. 146:4024-4030(1991).

"EMBL, M74139; AAA37776.1; -.

"Refervo; IPR0013599; Ig.

"InterPro; IPR0013599; Ig.

"Refervo; IPR0013599; Ig.

"Refervo; IPR00147; ig.].

"Refervo; IPR00147; ig.].

"Refervo; IPR00147; ig.].

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"Refervo; IPR00147; ig.].

"Refervo; IPR00147; ig.].

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"Refervo; IPR00147; ig.].

"Refervo; IPR00147; ig.].

"Refervo; IPR00147; ig.].

"Refervo; IPR00147; ig.].

"Refervo; IPR00147; ig.].
61 NQKFKGKATLITVDKSSSTAYMQLNSLTSEDSAVYYCARD---KDYYFDYWGQGTTLITVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 NQKFKDKAILTVDKSSTTAYMELRSLTSEDSAVYYCARSTMITNYVMDYWGQVTSVTVSS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 NQKFKGKATLIYUDKSSSTAYMQLNSLISEDSAVYYCARD---YSYVFDYWGQGTTLITVSS 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 EVQLQQSGPELVKPGASVKMSCKASGYTFTDYYMKWVKQSPGKSLEWIGDINPNNGGTSY
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                  25-0CT-2004 (TrEWBLrel. 28, Created)
25-0CT-2004 (TrEWBLrel. 28, Last sequence update)
25-0CT-2004 (TrEWBLrel. 28, Last annotation update)
Ab 126.33 heavy chain variable and joining regions (Fragment).
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Pred. No. 1.5e-31;
8; Mismatches 13; Indels
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Last annotation update)
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MEDLINE=91237115; Pubmed=1709665;
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80.0%;
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                                                                                                                                           PRELIMINARY;
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Q6PJA7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 NOKFKGKATLIVDKSSSTAYMELNSLISEDSAVYYCARYYYSGSYWYFDVWGAGTTVTVS 139
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 499; DB 2; Length 470;
Pred. No. 1.6e-31;
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Pred. No. 4.3e-32;
...matrhes 13; Indels
                                                                                                                 Strausberg R.; Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases. EMBL, BCO55910; AAH55910.1; -. HSSP; P01865; 1KB5.
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Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ225171; CAB65236.1; --
PIR; PH0973; PH0973.
                                                                                                                                                                                                   InterPro; IPR00110; Ig-like.
InterPro; IPR001597; Ig_c1.
InterPro; IPR0013697; Ig_c1.
InterPro; IPR001306; Ig_WHC.
InterPro; IPR001505; Ig_v.
Pfam; P07654; C1-set; 3.
SWART; SM00406; IGv; 1.
PROSITE; PS50815; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_1.
Hypothetical protein.
SEQUENCE 470 AA; 51727 MW; 6D90E4DF896BB090 CRC64;
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
Immunoglobulin heavy chain V-D-J region (Fragment).
                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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Matches 104; Conservative 11; Mismatches
                                                                 SEQUENCE FROM N.A. STRAIN=CZECH II; TISSUE=Mammary tumor;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig-v.
SMART; SM0406; IGv; 1.
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RA Parkes J., Helton E.K. Ketteman M., Madan A., Rodigues S., Sanhez A.,
RA Blakesley R.W., Touciman J.W., Madan A., Rodigues S., Sanhez A.,
RA Blakesley R.W., Touciman J.W., Green E.D., Dickson M.C.,
RA Krzywinski M.I., Skalska U., Schautz J., Whers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Schautz J., Whers R.M., Eutterfield Y.S.,
RA Jones S.J., Marra M.A.; analysis of more than 15,000 full-length human
RI Generation and Initial analysis of more than 15,000 full-length human
RI Generation and Initial analysis of more than 15,000 full-length human
RI Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
R. SEQUENCE FROM N.A.
R. SEQUENCE FROM N.A.
R. SUbmitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
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R. SWART; SMO0409; Ig-MHC.
R. SWART; SMO0409; IG-MHC.
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R. SWART; SMO0409; IG-MHC.
R. SWART; SMO0409; IG-MHC.
R. SROUENCE 472 AA; S2299 WM; IGSIGO23DSSDAAB CRC64;

Ouery Match
Bast Local Similarity 51.1%; Pred. No. 7e-31;
Ratches 112; Conservative 20; Mismatches 19; Indels 38; Gaps
Bast Local Similarity 51.1%; Pred. No. 7e-31;
Ratches 112; Conservative 20; Mismatches 19; Indels 38; Gaps
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Search completed: March 11, 2005, 14:55:45 Job time : 68 secs

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AF332008 Synthetic
A76868 Sequence 6
AR456298 Sequence 6
AK002242 Mus muscu
AX01550 Sequence
A3250760 Mus muscu
A3250760 Mus muscu
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A3564232 Synthetic
A3564232 Synthetic
A83227 Sequence 47
AR182952 Sequence
BD096925 Chemical
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AR182913 Sequence
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AK182944 Sequence
BD096917 Chemical
AX001511 Sequence
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AX001511 Sequence
CQ812173 Sequence
BD174830 ARtibody-
AX100174 Sequence
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OS Artificial Sequence

OS Artificial Sequence

Pr JP 2002507117-A/1

PD 05-MAR-2002

PF 04-UUN-1997 GB 9711579.4,20-JUN-1997 GB 9713150.2 PR

04-UUL-197 GB 9711579.4,20-JUN-1997 GB 9713150.2 PR

04-UUL-197 GB 9714230.1

PI SUSAN MARY KINGSMAN, CHRISTOPHER ROBERT BEBBINGTON, FIONA PI

MARGARET BLAED.

PI MILES WILLIAM.

PI MILES WILLIAM.

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PI ALTIFICIAL Sequence: DNA FR Key

Location/Qualifiers

FT source

/organism='Artificial Sequence'.
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                                                                                                                                                                                                                                                                                                                                                                                                 other sequences; artificial sequences.
1 (bases 1 to 729)
Kingsman, S.M., Bebbington, C.R., Ellard, F.M., Carroll, M.W. and
Myers, K.A.
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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                 A76868
AR456298
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SOURCE
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LOCUS
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BEBBINGTON CHRISTOPHER ROBERT (GB); CARROLL MILES WILLIAM (GB);
ELLARD FIONA MARGARET (GB); KINCSMAN SUSAN MARY (GB); MYERS KEVIN
ALAN (GB); OXFORD BIOMEDICA LTD (GB)
Location/Qualifiers
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other sequences; artificial sequences. . .
1 (Dases 1 to 729)
Stratford, I.J., Patterson, A.V., Kingsman, S.M., Kan, O., Griffiths, L.
and Mitrophanous, K.
Enhancement of produg activation
Patent: JP 2002505341-A 21 19-FEB-2002;
OXFORD BIOMEDICA LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IAN JAMES STRATFORD, ADAM VORN PATTERSON, SUSAN MARY KINGSMAN, ON
                                                                                                                                                              PAT 18-SEP-2002
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661 TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
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A61K47/48, A61K35/76, A61K38/44, A61K45/00, A61K48/00, A61P9/10,
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Description of Artificial Sequence: Synthetic sequence
Docation/Qualifiers
source 1.729
/organism='Artificial Sequence'.
Location/Qualifiers
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/organism="synthetic construct"
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/db_xref="taxon:32630"
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Enhancement of prodrug activation.
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PD 19-200250341-A/21
PD 19-FEB-2002
PF 05-MAR-1999 JP 2000534657
PR 06-MAR-1998 GB 9804841.6
29-JAN-1999 GB 9902081.0
PI IAN JAMES STRAIFORD, ADAM VOI
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JP 2002505341-A/21.
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721 ATCAAACGG 729
                                      721 ATCAAACGG
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PC C12NS
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/organism="synthetic construct"
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                                                                                                                              synthetic construct other sequences.
                                                                                                                                                                                                                                       Patent: WO 0136486-A 5 25-MAY-2001;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
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5 from Patent WO0136486.
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Kingsman, S.M., Mitrophanous, K., Patterson, A.V., Stratford, I.J., Griffiths, L. and Kan, O.
Enhanced product activation
Patent: WO 9945126-A. 26 ID-SEP-1999,
KINGSWAN SUSAN MARY (GB); MITROPHANOUS KYRIACOS (GB); PATTERSON
ADAM VORN (GB); STRATFORD IAN JAMES (GB); GRIFFITHS LEIGH (GB); KAN
ON (GB); OXFORD BIOMEDICA LTD (GB)
Location/Qualifiers
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
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Enhanced prodrug activation
Patent: WO 9945127 A 26 10-SEP-1999;
KINGSMAN SUSAN MARY (GB); MITROPHANOUS KYRIACOS (GB); PATTERSON ADAM VORN (GB); STRATFORD IAN JAMES (GB); GRIFFITHS LEIGH (GB); ON (GB); OXFORD BIOMEDICA LTD (GB)
Location/Qualifiers
   CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC
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larity 99.9%; Pred. No. 4.8e-219;
Conservative 0; Mismatches 1;
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/organism="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
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//mol.type="genomic DNA"
/mol.type="genomic DNA"
/db_xref="taxon:32630"
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                                WILES WILLIAM CARROLL, KEVIN ALAN MYERS C12N15/85, A61K48/00
Description of Artificial Sequence: CDN Key
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Pred. No. 5.2e-219;
0; Mismatches 1;
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1 (bases 1 to 1807)
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1 (bases 1 to 1467)
Kingsman,S.M., Bebbington,C.R., Ellard,F.M., Carroll,M.W. and
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    Aorganise="synthetic_construct"
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PR 04-JUN-1997 GB 9711279.4

O4-JUL-1997 GB 9711279.4

PI SUSAN MARY KINGSMAN, CHRISTOI

MARGARET ELIARD,

PI MILES WILLIAM CARROLL, KEVIN

PC C12N15/85,A61K48/00

CC Description of Artificial Sef

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                                                                                                                                                                                                                                                                                                                                                              Patent: WO 9855607-A 2 10-DEC-1998;
BEBBINGTON CHRISTOPHER ROBERT (GB); CARROLL MILES WILLIAM (GB);
ELLARD FIONA MARCARET (GB); KINGSMAN SUSAN MARY (GB); MYERS KEVIN
ALAN (GB); OXFORD BIOMEDICA LTD (GB)
Location/Qualifiers
1. 1807
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                                                                                                                                                                                                                                                                                 Bebbington, C.R., Carroll, M.W., Ellard, F.M., Kingsman, S.M. and
Myers, K.A.
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                             DNA
                                                                                                                                                                 synthetic construct
synthetic construct
other sequences; artificial sequences.
                 Sequence 2 from Patent W09855607. AX002779
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                                               DEFINITION
ACCESSION
VERSION
KEYWORDS
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Qy 121 CATGGAAGAGCCTTGAGTGGATTGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180 Db 859 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 918 Qy 181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCCAC	Qy 301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360	Oy 361 GGFGGTGGTGGAGGGTGGTGGCGCGCCGCGGATCTAGTATTGTGATGACC 420 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGACAGGGTTACCATAACCTGCAAGGCC 480 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 481 AGTCAGAGTGTGAGTAATGATGTAGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 540 Db 1219 AGTCAGAGTGTGAGTATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA 1278	Qy 541 CTGCTCATATCCTATACATCCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT 600	Qy 601 GGATATGGGACTTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660 Db 1339 GGATATGGGACTTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 1398	Qy 661 TATTCTGTCAGCAAGATTATAAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720 Db 1399 TATTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 1458	Oy 721 ATCAAA 726 Db 1459 ATCAAA 1464	RESULT 10 AX002780 LOCUS AX002780 LOCUS DEFINITION Sequence 3 from Patent W09855607. ACCESSION AX002780.1 GI:9885107	_		L Patent: W BEBBINGTO ELLARD FI ALAN (GB)	rce	CDS 11467 /note="unnamed protein product" /codon_start=1 /transl_table=11

and

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Date: JP 2002507117-A 5 05-MAR-2002;

OXFORD BIOMEDICA LTD
OS Artificial Sequence
DN JP 2002507117-A/5
PN JP 2002507117-A/5
PN JP 2002507117-A/5
PP 04-JUN-1996 JP 1999501858
PR 04-JUN-1997 GB 9714230.1
PR 04-JUN-1997 GB 9714230.1
PI SUSAN MARY KINGSMAN, CHRISTOPHER ROBERT BEBBINGTON, FIONA PI MARGARET ELLARD,
PI MILES HILLIARD,
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CC Description of Artificial Sequence: DNA FH Key
FH Key
I. 1518
FT source
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                                                                                                                        PAT 18-SEP-2002
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                                                                                                                                                                                                                                           other sequences; artificial sequences.
1 (bases 1 to 1518)
Kingsman, S.M., Bebbington, C.R., Ellard, F.M., Carroll, M.W.
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Location/Qualifiers
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larity 99.6%; Pred. No. 5.3e-218;
Conservative 0; Mismatches 3;
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JP 2002507117-A/5.
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synthetic construct
                             1459 ATCAAA 1464
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Matches 726; Conserv
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                                                                                                                                     Kingsman, A.O., Kingsman, S.M., Bebbington, C.R., Carroll, M.W. Ellard, F.M. and Myers, K.A.
Antibodies
Patent: WO 0136486-A 7 25-MAY-2001;
Oxford Blomedica (UK) Limited (GB)
Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="texon.32630"
/note="B7-1.5T48cFv.1"
                                                                                                      other sequences; artificial sequences
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Sequence 7 from Patent WO0136486
                                      GI:14347985
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ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACGTCTCCTCA
                                                                                                            ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTCA
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                                                                                                                                                                              GGTGGTGGGGGGGGGGCGCGCGCGCGGGGGGGGATCTAGTATTGTGATCC
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99.3%; Score 724.2; DB 6;
Best Local Similarity 99.6%; Pred. No. 5.3e-218;
Matches 726; Conservative 0; Mismatches 3;
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Patent: WO 0136486-A 11 25-WAY-2001;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
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AXI49550
AXI49550.1 GI:14347988
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BEBBINGTON CHRISTOPHER ROBERT (GB); CARROLL MILES WILLIAM (GB);
ELLARD FIONA MARGARET (GB); KINGSMAN SUSAN MARY (GB); MYERS KEVIN
ALAN (GB); OXFORD BIOMEDICA LTD (GB)
Location/Qualifiers
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                                                                                                                               AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA
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Pred. No. 5.3e-218;
0; Mismatches 3;
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/organise="synthetic construct"
/mol type="unassigned DNA"
/db_xref="taxon:32630"
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Sequence 5 from Patent WO9855607.
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Antibodies
Patent: WO 0136486-A 8 25-MAY-2001;
Oxford Biomedica (UK) Limited (GB)
Location/Qualifiers
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/mol_type="unassigned DNA"
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/db_xref="taxon:32630"
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GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGGCTTCAGTGAAGATA

cch 98.9%; Score 721; DB 6; Length 1796; al Similarity 99.3%; Pred. No. 5.6e-217; 724; Conservative 0; Mismatches 5; Indels

Query Match Best Local Matches 72

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8127.103 Million cell updates/sec
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Aax01652 Bispecifi
Ada3004 DNA encod
Abr1584 Anti-huma
Aaf30723 Anti-FIX/
Abx1364 Mouse rec
Adr28056 Polynucle
Adx13464 DNA encod
Acc57513 Newcastle
Abx12671 Venestle
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Aax77247 Mouse scF
Abx2322 VBGF bind
Aax77243 Mouse scF
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Adx18246 Mouse VBG
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ALIGNMENTS

RESULT 1

ADC79233 ADH34695 ADH34699

AAF30730 AAF30729

Tumour interacting protein; cancer; gene therapy; vector; ST4 antigen; monoclonal antibody; single chain antibody; scFv; mouse; 5T4scFv.1; ss Myers KA; Carroll MW, Murine anti-5T4 antigen monoclonal antibody scFv DNA. Bebbington CR, Ellard FM, ВР (OXFO-) OXFORD BIOMEDICA UK LTD 97GB-00011579. 97GB-00013150. 97GB-00014230. AAV80290 standard; cDNA; 729 98WO-GB001627 (first entry) 04-JUN-1997; 20-JUN-1997; 04-JUL-1997; WO9855607-A2 04-JUN-1998; 15-MAR-1999 10-DEC-1998. Mus sp. Synthetic. AAV80290; Chimeric. AAV80290

Kingsman SM,

WPI; 1999-059910/05. P-PSDB; AAW86002.

New vector encoding a tumour interacting protein for treating cancer - contains a desired nucleotide sequence and/or protein which recognises tumours, and is used as a gene delivery system to treat cancer.

Example 1; Fig 1A; 82pp; English.

This DNA sequence encodes a 5T4 scFv, designated 5T4scFv.1 (see AAW86002), comprising the heavy chain variable region (VH) from the murine 5T4 monoclonal antibody followed by a 15-amino acid flexible

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries N_Geneseq_16Dec04:* 1: qeneseqn1980s:* Database

Total number of hits satisfying chosen parameters:

US-10-016-686-5 729

Title: Perfect score:

Sequence:

Scoring table:

Searched:

seq length: 0 seq length: 200000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description	Aav80290 Murine an Aaf89729 Nucleotid Aaz19786 Anti-1574 Aaz07810 574 8cFv Aav80291 Anti-574 Aaf89730 Nucleotid Aav8029 Human B7- Aaf89730 Nucleotid Aav8029 ScFv-1gE1 Aaf89733 Nucleotid Aav80295 ScFv-1gE1 Aaf89733 Nucleotid Aav80295 ScFv-1gE1 AAf89732 Nucleotid Aav80295 ScFv-1gE1 AAf8670322 Polioviru Adf85425 V1228cFv Aav01651 Bispecifi Aav10378 Anti-CD86 Aav72072 Fusion pr Aav72072 Fusion pr Aav72059 Plasmid p Aav72064 Fusion pr
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and the light chain variable region (VL) of the mouse
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antibody. The trophoblast cell surface antigen defined by monoclonal antibody. The trophoblast cell surface antigen defined by monoclonal antibody 574 is expressed at high levels on the cells of a wide variety of human tumours. The 574serv.1 DNA sequence can be used to construct single-chain antibodies (see AAV80291) and scfv fusion constructs (see AAV80292-96). The invention relates to a vector comprising a nucleotide sequence coding for a tumour interacting protein (TIP) and optionally a nucleotide sequence of interest (NOI) which encodes a protein of interest (POI), the vector being capable of delivering the NOI and/or POI to the tumour recognised by the TIP. Delivery can be in vivo or ex vivo. The vector is used to treat cancer, and may also used as a gene delivery system for introducing at least 1 gene encoding a TIP (preferably a tumour binding protein) into a haematopoietic cell lineage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.9%; Score 728.2; DB 2; Length 729; 100.0%; Pred. No. 2.1e-197; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 729 BP; 180 A; 178 C; 189 G; 181 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.98;
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nes 729; Conservative
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The specification describes the use of a single chain antibody (ScFv), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The ScFv antibody is useful in the manufacture of a medicament, for affecting a disease in vivo, for preparing a pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The ScFv antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune disease, paridonnal diseases, cardiopulmonary diseases, ardiovascular diseases, gastrointestinal diseases, inflections, diabetes, Helicobacterrelated diseases, and other immune disorders. The present sequence encodes a ST4 ScFv of the invention. The antibody comprises the W and VI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regions from murine 5T4 monoclonal antibody, joined by a linker sequence
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                                                                                                                                                    Single chain antibody, ScFv; inflammatory disease; arthritis, cancer; hypersensitivity; autoimmune disease; central nervous system disorder; Parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                       /*tag= a
/transl_except= (pos: 505. .507, aa: Ala)
                                                                                                                      Nucleotide sequence of a 5T4 ScFv designated 5T4ScFv.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carroll MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99.9%; Score 728.2; DB 4; ilarity 100.0%; Pred. No. 2.1e-197; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kingsman A, Kingsman SM, Bebbington CR,
                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1. .729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (OXFO-) OXFORD BIOMEDICA UK LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-GB003859.
2000GB-00003527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000GB-00005071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-NOV-2000; 2000WO-GB004317
              AAF89729 standard; DNA; 729
                                                                                   (first entry)
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02-MAR-2000;
                                                                                     23-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAY-2001
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This sequence represents an example of a DNA encoding a secreted single chain antibody FV fragment, which is involved in transcellular localisation. In this example, the antibody is directed against the ST4 antigen. A secreted single chain antibody FV fragment can be fused to cytochrome P450 reductase (P450R) derivatives such as anchorless P450R (AAV4228F) or FV fragment (AAV4228F). This enables the fusion protein to be delivered to other cells where it is then transported to the mucleus. Wany drugs' sites of action are in the nucleus, rather than the cytoplasm, where P450R normally functions. P450R or its derivatives can be used to activate prodrugs to their active form via reduction. Administration of a prodrug is useful where the active drug may be metabolised before it reaches its site of action or where the active drug is cytotoxic, e.g., anticancer drugs. Targetted delivery of such cativators allows a reduction in dose of the prodrug, and thus of activators allows a reduction in dose of the prodrug, and thus of activators allowe a reduction in dose of the prodrug, and thus of activators allowe a reduction in dose of the prodrug, and thus of activators allowers, especifically used to treat tumours, inflammation, atherosclerosis and muscular dystrophy, but may also be used to treat many other conditions, e.g., cerebral malaria, rheumatoid arthritis, or conditions associated with hypoxia, ischaemia or hypoglycemia, or to inflammatories, antineoplastic agents and diagnostic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACGTGAAGCCTGGGGGCTTCAGTGAAGATA
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                                                                                                                                                                                                                                                          New prodrug activating agent targeted to selected cells or tissues, particularly hypoxic cells, for treating e.g. tumors.
                                                                                                                                                            Kan O, Griffiths L;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 729 BP; 180 A; 179 C; 189 G; 181 T; 0 U; 0 Other;
                                                                                                                                                            Patterson AV, Kingsman SM,
                                                                                                                                                                                                                                                                                                          Example 9; Fig 3; 187pp; English.
                                                                                                                            (OXFO-) OXFORD BIOMEDICA UK LTD
                                                            98GB-00004841.
98GB-00018103.
99GB-00002081.
                               99WO-GB000674
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                                                                                                                                                                                                            WPI; 1999-551046/46.
P-PSDB; AAY42294.
                                                                                                                                                                            Mitrophanous K;
                                                              06-MAR-1998;
19-AUG-1998;
29-JAN-1999;
                                                                                                                                                             Stratford IJ,
                               05-MAR-1999;
10-SEP-1999
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/product= "Anti-5T4 secreted single chain antibody Fv
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Mitrophanous K;
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New prodrug activating agent targeted to selected cells or tissues, particularly hypoxic cells, for treating e.g. tumors or inflammation.

Example 9; Fig 3F; 149pp; English.

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The invention provides a new prodrug activating agent that comprises: (1)

a localization domain (LD; other than a tumor-selective antibody) and a
prodrug activating domain (PDD); (1i) at least one nucleic acid encoding
a cytcchrome P450 and under control of at least one constitutive or
inducible expression control sequence or (1ii) a modified hematopoietic
stem cell (MRLSC) containing at least one nucleic acid encoding a PAD and
under control of elements as in (ii). The prodrug activating agent or
vectors that express them, are specifically used to treat tumors,
inflammation, atherosclerosis and muscular dystrophy, but may also be
used to treat many other conditions, e.g. cerebral malaria, rheumatoid
arthritis, or conditions associated with hypoxia, hypoglycemia or
schemia, or to deliver antibiotics, antiviral agents, analgesics,
schemia, or to deliver antibiotics, antiviral agents and diagnostic
agents. LD optimize activity of PAD, e.g. by delivering it to selected
locations or by delivering it to neighboring cells (bystander effect),
effects. Nucleic acids encoding the agent may be expressed selectively in
hypoxic cells. The present sequence represents the DNA encoding the
chingle chain variable antibody fragment against the tumor antigen ST4
(ST4 scFv). ST4 scFv and a human P450 reductase derivative alp450R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATTTCTGTCAGCAAGATTATATATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGACTCCCACATTCCTGCTTGTTTCAGCAGAGACAGGGTTACCATAACCTGCAAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   549 AGTCAGAGTGTGAGTAATGATGTAGCTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            669 GGATATGGGACGGATTTCACTTTCACCATCAGGACTTTGCAGGCTGAAGACCTGGCAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATTTCTGTCAGCAAGATTATAATTCTCCCCCGACGTTCGGTGGAGGCACCAAGCTGGAA
                                                                                                                                               TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC
                                                                                                                                                                                                                                        AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC
                                                                                                                                                                                                                                                                                                                 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       crecricararcerarcearcecracecracerecerecerearcecrareecrace
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                                                                                                                                                                                                                                                                                                                                                                  ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTCAGAGTGTGAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA
                                                                           1 GAGGICCAGCITCAGCAGICTGGACCTGACCTGGTGAAGCCTGGGGGCTTCAGTGAAGATA
                                       Gaps
                                   ő
 Length 1807;
                                       Indels
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Score 727.4; DB 2;
Pred. No. 4.9e-197;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV80292 standard; cDNA; 1467 BP.
 99.8%;
llarity 99.9%;
Conservative
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ATCAAACGG 797
                      Local Similarity
les 728; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single chain antibody, ScFv; inflammatory disease; arthritis; cancer; hypersensitivity; autoimmune disease; central nervous system disorder; Parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.
                                                                                                            CAGACTCCCACATTCCTGCTTGTTTCAGCAGAGACAGGGTTACCATAACCTGCAAGGCC
                                                                                                                                                                                                  GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC
                                                                                   CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC
                                                                                                                                                                       AGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACA
                                                                                                                                                                                                                                                                                                                                           GGATATGGGACTTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT
                                                                                                                                                                                                                                                                                                                                                                                     1339 GGATATGGGACGGATTTCACTTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT
                                                                                                                                                                                                                                                                                                 1279 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of a B7-1.5T4.1 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kingsman SM, Bebbington CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF89730 standard; DNA; 1467 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OXFO-) OXFORD BIOMEDICA UK LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-NOV-2000; 2000WO-GB004317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAR-2000; 2000GB-00005071.
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/*tag= a
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P-PSDB; AAB83836.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This DNA sequence encodes B7-1.5T4.1 (see AAW86004), a fusion protein comprising the extracellular domain (amino acids 1-215) of human costimulatory molecule B7-1 joined via a flexible peptide linker to an scPv (see AAW86002) derived from murine 5T4 monoclonal antibody. The CDNA can be inserted into vector pCI to allow expression of the fusion protein in mammalian cells. The trophoblast cell surface antigen defined by 5T4 is ceptressed at high levels on the cells a wide variety of human tumours. The invention relates to a vector comprising a nucleotide sequence coding for a tumour interacting protein (TIP) and optionally a nucleotide sequence coding for a tumour interacting protein (TIP) and optionally a nucleotide sequence of interest (NOI) which encodes a protein of interest (POI), the vector being capable of delivering the NOI and/or POI to the tumour recognised by the TIP. Delivery can be in vivo or ex vivo. The vector is used to treat cancer, and may also used as a gene delivery system for introducing at least 1 gene encoding a TIP (preferably a tumour binding protein) into a haematopoletic cell lineage. B7-1 is expected to bind specifically to CD28 and CTLA-4 present on human T-cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                      New vector encoding a tumour interacting protein for treating cancer contains a desired nucleotide sequence and/or protein which recognises tumours, and is used as a gene delivery system to treat cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGGCTTCAGTGAAGATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  979 AridGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT
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                                                                                                                                                                                                                                                                                                                       Myers KA;
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 1467 BP; 394 A; 349 C; 352 G; 372 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                     Carroll MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                     Bebbington CR, Ellard FM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 5; Fig 2; 82pp; English.
                                                                                                                                                                                                                                                                           (OXFO-) OXFORD BIOMEDICA UK LTD
                                                                                                                                                                                                           97GB-00013150.
97GB-00014230.
                                                                                                                                               98WO-GB001627
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Matches 725; Conservative
                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-059910/05.
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                                                             WO9855607-A2
                                                                                                                                               04-JUN-1998;
                                                                                                                                                                                                                                                                                                                     Kingsman SM,
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Synthetic.
                      Chimeric.
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standardise OS field)
                                    1459 ATCAAA 1464
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721 ATCAAA 726
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15-MAR-1999
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                                                                       The specification describes the use of a single chain antibody (ScFv), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The ScFv antibody is useful in the manufacture of a disease medicament, for affecting a disease in vivo, for preparing a pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The ScFv antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune diseases, cancers, central nervous system disorders including Parkinson's
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                                                                                                                                                                                                                                                    disease, periodontal diseases, cardiopulmonary diseases, cardiovascular diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-teated diseases, and other immune disorders. The present sequence encodes a B7-1.574.1 fusion protein. This comprises the N-terminus of the 574 ScPv is fused after amino acid 215 of human B7-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 724.4; DB 4; Length 1467;
Pred. No. 3.3e-196;
0; Mismatches 1; Indels 0;
condition associated with disease associated molecule.
                                                                                                                                                                                                                                                                                                                                                                      Sequence 1467 BP; 394 A; 349 C; 352.G; 372 T; 0 U; 0 Other;
                                    Claim 8; Fig 2; 118pp; English.
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Best Local Similarity 99.9%;
Matches 725; Conservative (
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This DNA sequence encodes a fusion protein comprising the extracellular domain of mouse co-stimulatory molecule B7-1 joined via a flexible peptide linker to an scPv (see AAW86002) derived from murine ST4 monoclonal antibody. The fusion can be used to construct a recombinant vector, e.g. retrovirus, lentivirus, adenovirus, poxvirus, vaccinia virus trophoblast cell surface antigen defined by ST4 is expressed at high levels on the cells of a wide variety of human tumours. The invention relates to a vector comprising a nucleotide sequence coding for a tumour interacting protein (TIP) and optionally a nucleotide sequence of interacting protein (TIP) and optionally a nucleotide sequence of optionally a nucleotide sequence of the reacting protein (TIP) and optionally a nucleotide sequence of by the TIP. Delivery can be in vivo or ex vivo. The vector is used to treat cancer, and may also used as a gene delivery setum for introducing at least 1 gene encoding a TIP (preferably a tumour binding protein) into a hasmatopoietic cell lineage. B7-1 binds specifically to CD28 and CTLA-4 present on human CD4 and CD8 cells. (Updated on 17-OCT-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                       Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen; monoclonal antibody; single chain antibody; scFv; mouse; B7-1; co-stimulatory molecule; s8.
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                                                                                                                                                                                                                                                                                                 B7-1/scFv specific for use in cancer gene therapy.
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AAV80294 standard; cDNA; 1518 BP.
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                     TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC
                                             CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC
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                                                                                                                                                                                                                                                                                                                                                                                                                               Use of single chain antibody capable of recognizing a disease associated molecule for manufacturing a medicament for preventing and/or treating a disease condition associated with disease associated molecule.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 724.2; DB 4; Length 1518;
Pred. No. 3.8e-196;
0; Mismatches 3; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1518 BP; 398 A; 364 C; 371 G; 385 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGGCT
                                                                                                                                                                                                                                     Carroll MW,
                                                                                                                                                                                                                                     Kingsman SM, Bebbington CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 8; Fig 5; 118pp; English.
                                                                                                                                                         (OXFO-) OXFORD BIOMEDICA UK LTD
18-NOV-1999; 99WO-GB003859.-
15-FEB-2000; 2000GB-00003527.
                                                                            02-MAR-2000; 2000GB-00005071.
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hes 726; Conservative
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pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The ScFv antibody is also useful for treating inflammatory diseases including arthritis, hypersensitivity, autoimmune diseases, cancers, central nervous system disorders including Parkinson's disease, periodontal diseases, cardiopulmonary diseases, cardiovascular diseases, infections, diabetes, Helicobacterrelated diseases, and other immune disorders. The present sequence encodes an Ig-574 fusion protein
                                                                                                                                                                                                                                                                                                                                                  69 GAGGICCAGCIGCAGCAGTCIGGACCIGACCIGGIGAAGCCIGGGGCIICAGIGAAGAIA
                                                                                                                                                                                                                                                                                                                                                                                                                    129 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC
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                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                           Score 721; DB 4; Le
Pred. No. 3.3e-195;
                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.3
Matches 724; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Single chain antibody; ScFv; inflammatory disease; arthritis; cancer; hypersensitivity; autoimmune disease; central nervous system disorder; Parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.
                                                                                           CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT
                                                                                                                                                                                   1387 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT
                                                               CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCCAGT
                                                                                                                                             GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT
                                                                                                                                                                                                                              TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA
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/transl_except= (1518. .1520, aa: Met)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence of an Ig-5T4 fusion protein.
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12. .1790
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15-FEB-2000; 2000GB-00003527.
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P-PSDB; AAB83838
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single chain antibody; ScFv; inflammatory disease; arthritis; cancer; hypersensitivity; autoimmune disease; central nervous system disorder; Parkinson's disease; periodontal disease; cardiopulmonary disease; cardiovascular disease; gastrointestinal disorder; infection; diabetes; Helicobacter-related disease; immune disorder; ss.
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                                                                                                                                                                                                                                                                                                                                                                 CTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGT
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                                                                           ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACGTCTCTTCA
                                                                                                                 GGTGGTGGTGGGAGCGGTGGTGGCGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of a SvFv-IgE protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kingsman SM, Bebbington CR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF89734 standard; DNA; 2090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
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                                                                                             Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen; monoclonal antibody; single chain antibody; scFv; mouse; human; IgE1; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New vector encoding a tumour interacting protein for treating cancer - contains a desired nucleotide sequence and/or protein which recognises tumours, and is used as a gene delivery system to treat cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC
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                                                         ScPv-1gEl fusion construct for use in cancer gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carroll MW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 721; DB 2; I
Pred, No. 3.5e-195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ellard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 13; Page 64; 82pp; English.
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97GB-00013150.
97GB-00014230.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bebbington CR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.9%;
ilarity 99.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-059910/05.
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                                                                                                                                                                        Homo sapiens.
Synthetic.
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Local Sin
724; C
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                                                                                                                                                                                                                                                                                                                           04-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                 04-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                       04-JUL-1997;
                                                                                                                                                                                                                                                                                        10-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                     20-JUN-1997
                                                                                                                                                                                                              Chimeric.
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The invention comprises molecules that specifically bind to at least one intra- or extracellular domain of the poliovirus receptor (PVR) - also known as CDI55 (cluster of differentiation 155). The molecules of the invention have the ability to modulate receptor mediated adhesion, trafficking and/or invasion behaviour of a cell expressing PVR. The molecules of the invention are useful for the prevention and/or treatment of proliferative disorders, cancer or mecastrasis. The molecules of the invention are also useful for identifying agents that can modulate PVR-sequence encodes a PVR-specific scFv protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New molecules that modulate poliovirus receptor (PVR) mediated adhesion, trafficking and/or invasion behavior of a cell expressing CD155 or PVR, useful for preventing or treating proliferative disorders, such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 CAGCTTCAGCAGTCTGGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATATCCTGC
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                                                                                                                                                                                                                                                                                                            receptor mediated adhesion modulation;
cell traffitching behaviour modulation;
cell invasion behaviour modulation; proliferative disorder; cancer;
metaetasis; PVR-mediated adhesion; PVR-mediated invasion potential;
                                                                                                                                                                                                                                                                                          poliovirus receptor; PVR; CD155; cluster of differentiation 155;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jay DG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.6%; Score 463.6; DB 13; Length 804; 79.8%; Pred. No. 7.5e-122; tive 0; Mismatches 129; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 804 BP; 213 A; 197 C; 227 G; 167 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Torella C,
                                                                                                                                                                                                                                             Poliovirus receptor (PVR)-specific scF2 coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1. .804
/*tag= a /*partial /product= "PVR-specific scFv2 protein" /note= "No start codon is given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lain B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; SEQ ID NO 6; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zehetmeier C,
                                                                                                             BP.
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28-MAY-2003; 2003EP-00012314.
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                                                                                                           ADR70322 standard; DNA; 804
                                                                                                                                                                                                   (first entry)
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Matches 579; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Beste G, Z, Sloan KE;
  789 ATCAAACGG 797
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                                                                                                                                                                                                                                                                                                                                                                                                          scFv2; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                   18-NOV-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-SEP-2004
                                                                                                                                                       ADR70322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unger CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                          The specification describes the use of a single chain antibody (ScFv), which is capable of recognizing a disease associated molecule in the manufacture of a medicament for the prevention and treatment of a disease condition. The ScFv antibody is useful in the manufacture of a medicament, for affecting a disease in vivo, for preparing a pharmaceutical composition, for in vivo imaging and/or for adjuvant treatment of a disease. The ScFv antibody is also useful for treating inflammatory disease including arthritis, hypersensitivity, autoimmune disease, cancers, central nervous system disorders including Parkinson's disease, periodontal diseases, cardiopulmonary diseases, cardiovascular diseases, gastrointestinal disorders, infections, diabetes, Helicobacterrelated diseases, and other immune disorders. The present sequence encodes a ScFv of the invention linked to an IgE sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACCAGAAATTCAAGGACAAAGGCCATATTAACTGTAGACAAGTCATCCACCACCACGCCTAC 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     369 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACCGTCTCTTCA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         429 GGTGGTGGTGGAGCGGTGGTGGCGCCACTGGCGGCGGCGGATCTAGTATTGTGATGACC 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGACTCCCACATTCCTGCTTGTTTCAGCAGAGACAGGGTTACCATAACCTGCAAGGCC 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAA 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TATTTCTGTCAGCAAGATTATATATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTTGAA 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC
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0; Mismatches 5; Indels
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Matches 724; Conservative
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The present invention relates to mutated Fv library having mutations designed such that the amino acid at position K (k is integer 2≤k≤ 20) is introduced at amino acid position m (m is integer 2≤k≤(n-1)) chosen from a region consisting of n residues (n is integer 3≤n contained in complementarity determining regions (CDR) or other closer segions of an antibody, and forms limited Fv repetrory of (n n)C m &times ;km. The invention can be used for efficiently acquiring mutated antibody. The present sequence represents V122scFv clone encoding
                                                                                                                                                              Mutated Fv library useful for screening mutated Fv for preparation of mutated antibody for diagnostic purposes, having mutations at specific amino acid positions of complementarity determining regions of antibody
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                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 1; 17pp; Japanese
      (NISB ) JAPAN TOBACCO INC.
                                                                     2004-027982/03
                                                                                                      P-PSDB; ADF85426
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                                                                                                                                 CCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCC
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                                                                                                                                                                                                                                                                                                                                                 ATTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAAA
                                                                  AGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTTGGGGCTTCAGTGAAGATAT
                                                                                                                                                                                               ATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTTACA
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                                   Gaps
                                   18;
   Length 852;
                                 0; Mismatches 147; Indels
 DB 12;
 Score 446.8; DB 1
Pred. No. 4.8e-117
tch 61.3%;
al Similarity 77.3%;
563; Conservative
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encoding sequence

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710 ATTTCTGTGAGCAATACAGCAGCTCTCCGTATACGTTCGGATCGGGCACCAAGCTGGAAA 769
                                                                                                                                                                                                                                                                                                                                                                                                    B7 binding molecule; costimulatory molecule; B7.1; CD80; B7.2; CD86; T cell activation; inhibitor; graft versus host disease; transplant rejection; allograft rejection; autoimmune disease; allergy; therapy; human; bispecific tetravalent antibody; BiTAb; BiTAb; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New molecules which bind B7.1 and B7.2 - useful to prevent and treat
immune diseases including allograft rejection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers

1. 1726

/*tag= a
/*transl_except= (pos:780. .782, aa:Ile)
/transl_except= (pos:967. .969, aa:Xaa)
/note= "Xaa= Gln-Leu-Val-Gln-Val-Gln"
                                                                                                                                                                                                                                                                                                                                                            Bispecific tetravalent antibody BiTAbB724-IG10H6 DNA
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/note= "pelB signal sequence"
73. .1726
/*tag= c
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                                                                                                                                                                                                                 AAX01651 standard; DNA; 1725 BP.
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Synthetic.
Chimeric.
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                                                                                                                                 Gaps
                                                                                                                                 27;
                                                                                    Length 1725;
                                            Sequence 1725 BP; 424 A; 439 C; 468 G; 394 T; 0 U; 0 Other;
                                                                                    60.6%; Score 442; DB 2; Length 17.78.5%; Pred. No. 1.4e-115; ive 0; Mismatches 135; Indels
disease, allergy and autoimmune diseases (claimed)
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Job time : 538 secs
                                                                                  Query Match
Best Local Similarity 78.5
Matches 590; Conservative
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APPLICANT: Fleer, Reinhard
APPLICANT: Fleer, Reinhard
APPLICANT: Fournier, Alain
APPLICANT: Guitcon, Jean-Dominique
APPLICANT: Jung, Gerard
APPLICANT: Jung, Gerard
APPLICANT: Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
TITLE OF INVENTION: REPEARATION THEREOF AND PHARMACEUTICAL COMPOSITION
TITLE OF INVENTION: CONTAINING SAID POLYPEPTIDES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, 3C43
CCUNTRY: Collegeville
STATE: PA
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MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.1
SOFTWARE: Macintosh
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-0AN-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: US 08/256,927
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PR 92/01064
FILING DATE: 28-JUL-1994
APPLICATION NUMBER: PR 92/01064
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: PST$2006-US
TELECOMMUNICATION INFORMATION:
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TYPE: nucleic acid
STRANDEDNESS: double
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March 14, 2005, 18:41:00; Search time 190 Seconds (without alignments) 6278.135 Million cell updates/sec
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(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                            GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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ALIGNMENTS

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PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/797,689
FILING DATE: 31-JAN-1997
APPLICATION NUMBER: US 08/256,927
FILING DATE: 28-UUL-1994
APPLICATION NUMBER: PR 92/01064
FILING DATE: 31-JAN-1992
APPLICATION NUMBER: PCT/FR93/00085
FILING DATE: 28-JAN-1993
ATTORNEY/AGENT IRFORMATION:
NAME: Smith Ph.D., Julie K.
REGISTRATION NUMBER: P.38,619
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                          ADDRESSEE: Rhone-Poulenc Rorer Inc
STREET: 500 Arcola Road, 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: Macintosh
COMPUTER: Macintosh
OPERATIOS SYSTEM, System 7.1
SOFTWARE: Word 5.1 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/984,186
FILING DATE: 29-Oct-2001
CLASSIFICATION: <a href="https://doi.org/10.1007/10.1007/">doi.org/10.1007/</a>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: 3..752
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-984-186-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (610) 454-3839
                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (610) 454-3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 756 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 17: SEQUENCE CHARACTERISTICS:
                                                                                                               NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                               ZIP: 19426
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: CDNA
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Matches 572; Conservative
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                                                                                                                                                                                                                                                                                                   COUNTRY:
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                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                               Length 756;
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                                                                                                                                                                                                      Score 458.2; DB 2;
Pred. No. 3.5e-136;
0; Mismatches 153;
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Patent No. 6686179
GENERAL INFORMATION:
APPLICANT: Fleer, Reinhard
Guitton, Jean-Dominique
Jung, Gerard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAAGCTGGAAATCAAA 726
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                                                                                                                                                                                                      Query Match
Best Local Similarity 77.6%;
Matches 572; Conservative
                        MOLECULE TYPE: CDNA
TOPOLOGY: linear
                                                                                                                     3..752
                                                                                      CDS
                                                                                NAME/KEY:
; LOCATION:
US-08-797-689-17
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US-09-984-186-17
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Yeh, Patrice
TITLE OF INVENTION: NOVEL BIOLOGICALLY ACTIVE POLYPEPTIDES,
PREPARATION THEREOF AND PHARMACEUTICAL COMPOSITION
CONTAINING SAID POLYPEPTIDES ï 252 181 241 312 62 CCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGCC 121 ccriecaka derricreser a cearricas raserer resarea a crieda a de casa d 133 cridaacaddarcrirgagriggarriggacdagarrirarccriggagardgagaraccaaaraca 192 TGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTA 301 72 13 AGGTGCAGCTCCAGCAGTCTGGACCTGAGCTGAAGCCTGGGGCCTCAGTGAAGATTT 122 ATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAÇA ACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACCACGCTACA 2 AGGICCAGCITCAGCAGICTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATAI Gaps 12; Length 756; Indels 62.9%; Score 458.2; DB 4; 77.6%; Pred. No. 3.5e-136; 0; Mismatches 153;

us-10-016-686-5.rni

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                                                                                                                 2 AGGICCAGCITCAGCAGICTGGACCTGACCTGGTGAAGCCTGGGGCTTCAGTGAAGATAT
                                                                                                                                                                       68 AGGICCAACTGCAGCAGCCTGGGCCTGAACTGGTGAAGCCTGGGGGCTTCAGTGCAGCTGT
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                                                           Gaps
                                                        56;
Length 864;
                                                        Indels
Score 438.8; DB 3;
Pred. No. 6.1e-130;
0; Mismatches 137;
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Patent No. 6339070
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSER: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
STATE: D.C.
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  60.2%;
Query Match 60.2
Best Local Similarity 78.3
Matches 587; Conservative
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US-09-423-439-31
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FILING DATE: 09-No. 6339070-1999
CLASSIPICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 47:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 47, Application US/09423439;
Patent No. 6339070
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CHEMICAL COMPOUNDS
INUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Winthrop, L.L.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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MOLECULE TYPE: other nucleic acid

SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-09-423-439-47
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LENGTH: 864 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                            718 CAGGCTGAAGACCTGGCAATTTATTACTGCAAGCCATCTTATA---CTCTTCGGACGTTC 774
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640 CAGGCIGAAGACCTGGCAGTTTATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Fillsbury Winthrop, L.L.P. STREET: 1100 New York Ave., N.W. CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-No. 6339070-1939
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
                                                                                       700 GGTGGAGGCACCAAGCTGGAAATCAAACGG 729
                                                                                                                 775 GGTGGAGCACCAAGCTCGAGATCAAACGG 804
                                                                                                                                                                                                                                     Sequence 37, Application US/09423439
Patent No. 633970
GENERAL INFORMATION:
GENERAL INFORMATION:
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: GB 9709421.3 FILING DATE: 10-MAY-1997 INFORMATION FOR SEQ ID NO: 37: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-09-423-439-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 05-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
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STRANDEDNESS: single
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ZIP: 20005
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 438.8; DB 3;
Pred. No. 9.7e-130;
0; Mismatches 137;
           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
ONDERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRING APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-NO. 6339070-1999
CLASSIFICATION: <URKNOWN>
PRIOR APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: other nucleic acid SEQUENCE DESCRIPTION: SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2019 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 78.3%;
Matches 587; Conservative (
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RESULT 7
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is Sequence 5, Application US/10096246A
jeach No. 6818748
igenerate No. 6818748
igenerate INFORMATION:
APPLICANT: Pulton, R. Elaine
APPLICANT: Nagata, Leslie
APPLICANT: Alvi, Azhar Z.
ITILE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of
ITILE OF INVENTION: Used (VEE)
ITILE OF INVENTION: Virus (VEE)
ITILE OF INVENTION: Virus (VEE)
ITILE OF INVENTION: Virus (VEE)
CURRENT FELLING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 777
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Pred. No. 1.9e-124;
1; Mismatches 166;
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OTHER INFORMATION: 8cFv protein MA116-14 1 - 720
OTHER INFORMATION: e-tag 721 - 777
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NAME/KEY: CDS
LOCATION: (1).
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Best Local S:
Matches 546
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APPLICANT: The Minister of National Defence, Government of Canada
APPLICANT: The Minister of National Defence, Government of Canada
APPLICANT: Pulton, R E
APPLICANT: Nagata, Leslie
APPLICANT: Nagata, Leslie
TITLE OF INVENTION: Serve Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
FILE REFERENCE: NEL-007
CURRENT APPLICATION NUMBER: US/10/092,246
CURRENT APPLICATION NUMBER: US/10/092,246
CURRENT PILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.1
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  -CTATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCC 357
                                                                                        TCAGGTGGTGGTGGGGGGGGGGGGGGCACTGGCGGCGGCGGATCTAGTATTGTGATG 417
                                                                                                                                 418 TCAGGTGGCGGTGGCTCGGGCGGTGGTCGGGTCGGGTGGCGGGATCTGACATTGAGCTC 477
                                                                                                                                                                          ACCCAGACTCCCACATTCCTGCTTCTTCAGCAGGACAGGGTTACCATAACCTGCAAG 477
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                                    359 CCTATGGTTACG-ACGATGCTATGGACTACTGGGGCCCAAGGGACCACGGTCACCGTCTCC
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5 Sequence 5, Application US/10092246
7 Patent No. 6501314
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1; Mismatches 169;
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Local Similarity 74.6%;
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Patent No. 6501314

GENERAL INFORMATION:
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APPLICANT: The Minister of National Defence, Government of Canada
APPLICANT: The Minister of National Defence, Government of Canada
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APPLICANT: Negata, Lesite
TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of MC
TITLE OF INVENTION: ScrV Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
FILE REFERENCE: NEL-0007
CURRENT FILING DATE: 2002-03-13
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 7
ILENGHT: 777
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; ORGANISM: Mouse hybridoma cell line 1A4A1
US-10-092-246-7
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APPLICANT: Fulton, R. Elaine
APPLICANT: Nagata, Leslie
APPLICANT: Nagata, Leslie
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APPLICANT: Nagata, Leslie
APPLICANT: Nagata, Leslie
APPLICANT: Nation Cloning, Expression, Sequencing, and Functional Enhancement of
TITLE OF INVENTION: Cloning (VEE)
TITLE OF INVENTION: Virus (VEE)
TITLE OF INVENTION: Virus (VEE)
TITLE OF INVENTION: Virus (VEE)
TITLE OF INVENTION: Virus (VEE)
TITLE OF INVENTION: Virus (VEE)
TITLE OF INVENTION: VIRUS (VEE)
TITLE OF INVENTION NUMBER: US/10/096,246A
CURRENT APPLICATION NUMBER: US/10/096,246A
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin version 3.2
SEQ ID NO 7
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US-09-581-345-1
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                                                                                                                   Length 777;
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                                                                                                                   Score 416.8; DB 4;
Pred. No. 6.4e-123;
1; Mismatches 169;
                                                                     - 720
                                                                   OTHER INFORMATION: scrv protein MA116-15 1
OTHER INFORMATION: e-tag 721 - 777
                                                                                                                     57.2%;
                                                                                                                                 Best Local Similarity 74.6
Matches 543; Conservative
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           TYPE: DNA
ORGANISM: mouse
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NAME/KEY: CDS
LOCATION: (1).
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Sequence 1, Application US/09581345; Patent No. 6809184; GENERAL INFORMATION:

RESULT 10 US-09-581-345-1

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APPLICANT: Chowdhury, Partha S.
APPLICANT: The Government of the United States
APPLICANT: The Government of the United States
APPLICANT: as represented by The Secretary of the
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Immunoconjugates Having High Binding Affinity for
TITLE OF INVENTION: Mesothelin and Methods for Their Use
FILE REFERENCE: 015280-339100US
CURRENT PAPLICATION NUMBER: US/09/581,345
CURRENT PILING DATE: 2000-09-27
PRIOR PAPLICATION NUMBER: WO 60/067,175
PRIOR APPLICATION NUMBER: WO PCT/US98/25270
PRIOR APPLICATION NUMBER: WO PCT/US98/25270
PRIOR PILING DATE: 1999-11-25
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 1
LENGTH: 723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence:SS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 413.8; DB 4;
Pred. No. 5.6e-122;
1; Mismatches 174;
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Best Local Similarity 75.0%;
Matches 544; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
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                                 GATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTT
                                                                                                                                            ATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCAAGCTGGAAA
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Pred. No. 2.2e-121;
1; Mismatches 172; Indels
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NAME/KEY: CDS
LOCATION: (1)..(777)
OTHER INFORMATION: SCFV protein MA116-16
OTHER INFORMATION: e-tag
721 - 777
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74.2%;
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Best Local Similarity 74.2
Matches 540; Conservative
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ORGANISM: mouse
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US-10-096-246A-6
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Barent No. 6501314

GENERAL INFORMATION

APPLICANT: The Minister of National Defence, Government of Canada

APPLICANT: The Minister of National Defence, Government of Canada

APPLICANT: Alvi, Azhar E

APPLICANT: Alvi, Azhar E

APPLICANT: Nagata, Lesile

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APPLICANT: Nagata, Lesile

APPLICANT: Nagata, Lesile

APPLICANT: NAMBER: USFV Antibody Against Venzuelan Equine Encephalitis Virus (Vee)

FILE REFERENCE: NEL-007

CURRENT APPLICATION NUMBER: US/10/092,246

CURRENT FILING DATE: 2002-03-13

NUMBER OF SEQ ID NOS: 37

SOFTWARE: PatentIn version 3.1
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1; Mismatches 172; Indels
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US-10-092-246-6
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JUNEAREAL INCOMENTATION:

JUNEARAIL INCOMENT. Cheung, Nai-Kong V.

APPLICANT: Larson, Steven M.

APPLICANT: Larson, Steven M.

APPLICANT: Rivilin, Ken

JUNEARIT: Rivilin, Ken

TITLE OF INVENTION: Single Chain FV Constructs of Anti-Ganglioside GD2

TITLE OF INVENTION: Antibodies

TITLE OF INVENTION: Antibodies

FILE REFERENCE: MSK.P-013-USNP

CURRENT FILING DATE: 1998-09-18

PRIOR APPLICATION NUMBER: 05/09/1427

PRIOR APPLICATION NUMBER: 60/013,703

PRIOR PILING DATE: 1996-03-20

PRIOR FILING DATE: 1996-03-20

NUMBER OF SEQ ID NOS: 5

SOFTWARE: Patentin Ver. 2.1

SEQ ID NOS: 5
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                                                                                                                                                                              302 TGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCAG 361
                                         182 AGCAGAAAGTTCAAGGCCAAGGCCACATTGACTGTAGACAAGTCCTCCAGCACAGCCTACA
                                                                                                                                 242 TGGAGCTCCGCAGCCTGACATCTGAGGATTCTGCAGTCTATTACTGTGCAAGAGATACTA
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ORGANISM: Murine
PEGANISM:
OTHER INFORMATION: 5F11-scFv-streptavidin
NAME/KEY: unsure
LOCATION: (37)
LOCATION: (79)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09142974B; Patent No. 6451995; GENERAL INFORMATION: APPLICANT: Cheung, Nai-Kong V.
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APPLICANT: Cheund, Steven M.
APPLICANT: Cheund, Steven M.
APPLICANT: Larson, Steven M.
APPLICANT: Riviin, Ren
APPLICANT: Riviin, Ken
APPLICANT: Sadelain, Michel
TITLE OF INVENTION: Single Chain FV Constructs of Anti-Ganglioside GD2
TITLE OF INVENTION: Single Chain FV Constructs of Anti-Ganglioside GD2
TITLE OF INVENTION: Antibodise
FILE REFERENCE: MSK.P-013-USNP
CURRENT APPLICATION NUMBER: US/09/142,974B
CURRENT FILING DATE: 1996-09-18
PRIOR FILING DATE: 1997-03-20
PRIOR PLICATION NUMBER: 60/013,703
PRIOR PLICATION NUMBER: 60/013,703
PRIOR PLING DATE: 1996-03-20
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 717
  481
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                                                                                                   473 GTCAGGATGTGGATACTGCTGTAGGCTGGTATCAACAGAGACCAGGGCAATCTCCTAAAC 532
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                                                                             GTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGGGCAGTCTCCTACAC
                        542 IGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGATCGCTTCATTGGCAGTG
  AGACTCCCACATTCCTGCTTGTTTCAGCAGGACAGGGTTACCATAACCTGCAAGGCCA
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Pred. No. 5.1e-121;
1; Mismatches 171;
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ORGANISM: Murine
FEATURE:
OTHER INFORMATION: 5F11-scFv
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LOCATION: (37)
NAME/KEY: unsure
LOCATION: (79)
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SOFTWARE: Pat
SEQ ID NO 4
LENGTH: 777
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Batent No. 6501314
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: The Minister of National Defence, Government of Canada
APPLICANT: Alvi, Azhar E
APPLICANT: Najas, Leslie
TITLE OF INVENTION: Cloning, Expression, Sequencing, and Functional Enhancement of MC
TITLE OF INVENTION: ScFv Antibody Against Venzuelan Equine Encephalitis Virus (Vee)
FILE REFERENCE: NEL-0007
CURRENT APPLICATION NUMBER: US/10/092,246
CURRENT FILING DATE: 2002-03-13
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                                                                                          Gaps
                                                                                          12;
                                            Length 1176;
                                                                                                                                    AGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCTGGGGCT
                                                                                          Indels
                                         Score 410.8; DB 3;
Pred. No. 6.7e-121;
1; Mismatches 171;
                                         56.4%;
ilarity 74.7%;
Conservative
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                                                                Similarity
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Best Local Simi
Matches 544;
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US-10-092-246-4
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; CIHER INFORMATION: DNA encoding a 5T4 scFv, designated 5T4scFv.1 US-10-334-235-1
                                                                                                                                                                                                                                                                                                                                                                       99.9%; Score 728.2; DB 18;
100.0%; Pred. No. 1.1e-224;
ive 0; Mismatches 0;
               FILE REFERENCE: 532682000920
CURRENT APPLICATION NUMBER: US/10/334,235
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: US 10/660,585
PRIOR FILING DATE: 2002-01-29
PRIOR FILING DATE: 2000-11-13
PRIOR PLILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: US 09/445,375
PRIOR FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 729
 TITLE OF INVENTION: VECTOR SYSTEM
                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 729; Conservative
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Publication No. US20040131591A1
GENERAL INFORMATION:
APPLICANT: Kingsman, Alan
APPLICANT: Ringsman, Christopher
APPLICANT: Carroll, Miles
APPLICANT: Ringsman, Susan
APPLICANT: Ringsman, Susan
APPLICANT: Kingsman, Susan
APPLICANT: Kingsman, Susan
APPLICANT: Lamikandra, Roini
APPLICANT: Lamikandra, Abigail
; OTHER INFORMATION: 5T4 SCFv
US-10-060-585-1
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Pred. No. 2.9e-224;
0; Mismatches 1;
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PRIOR APPLICATION NUMBER: US 09/445375

PRIOR FILING DATE: 1998-06-04

PRIOR PILING DATE: 1998-06-04

PRIOR PILING DATE: 1997-06-09

PRIOR PILING DATE: 1997-06-20

PRIOR PILING DATE: 1997-06-20

PRIOR FILING DATE: 1997-06-20

PRIOR FILING DATE: 1997-06-30

PRIOR FILING DATE: 1997-07-04

PRIOR FILING DATE: 1997-07-04

PRIOR PILING DATE: 1997-07-04

PRIOR PILING DATE: 1997-07-04

PRIOR PILING DATE: 1997-07-04

PRIOR PILING DATE: 1999-11-13

PRIOR FILING DATE: 1999-11-16

NUMBER OF SEQ ID NOS: 27

SOFTWARE: FASTESEQ for Windows Version 4.0

SENGTHAL: 1807
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/10060585
Publication No. US20030083290A1
GENERAL INFORMATION:
APPLICANT: Kingsman, Alan J.
APPLICANT: Bebbington, Christopher R.
APPLICANT: Carroll, Miles W.
APPLICANT: Kingsman, Susan M.
APPLICANT: Kingsman, Susan M.
APPLICANT: Kingsman, VECTOR SYSTEM
TITLE OF INVENTION 'VECTOR SYSTEM
FILE REFERENCE DYOUZ3.001CF1
CURRENT APPLICATION NUMBER: US/10/660,585
CURRENT FILING DATE: 2002-0-06
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Best Local Similarity 99.9%;
Matches 728; Conservative
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US-10-060-585-2
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US-10-060-585-2
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; OTHER INFORMATION: Coding sequence of 5T4scFv
US-10-787-881A-1
                                                                                                                                                                                                                                APPLICANT: Kingsman, Susan M.
APPLICANT: Bebbington, Christopher R.
APPLICANT: Bland, Fiona M.
APPLICANT: Bland, Fiona M.
APPLICANT: Carroll, Miles W.
APPLICANT: Carroll, Wiles W.
APPLICANT: Myers, Kevin A.
TITLE OF INVENTION: Vector
FILE REFERENCE: 021911-000330US
CURRENT APPLICATION NUMBER: US/10/787,881A
CURRENT APPLICATION NUMBER: US 09/445,375
PRIOR APPLICATION NUMBER: US 09/445,375
PRIOR APPLICATION NUMBER: PCT/GB98/01627
PRIOR PILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 24
NUMBER OF SEQ ID NOS: 24
                                                                                                                                          Sequence 1, Application US/10787881A Publication No. US20050032216A1 GRNERAL IPPORMATION: APPLICANT: Oxford BioMedica (UK) Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
SEQ ID NO 1
LENGTH: 729
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Sequence 2, Application US/10787881A
Publication No. US20050032216A1
GENERAL INFORMATION:
APPLICANT: Oxford BioMedica (UK) Ltd.
APPLICANT: Kingsman, Susan M.
APPLICANT: Blabington, Christopher R.
APPLICANT: Blabington, Christopher R.
APPLICANT: Bland, Fiona M.
APPLICANT: Carroll, Miles W.
APPLICANT: Carroll, Miles W.
TITLE OF INVENTION: Vector
FILE REFERENCE: 021911-000330US
CURRENT APPLICATION NUMBER: US/10/787,881A
CURRENT FILING DATE: 2004-02-25
FRIOR APPLICATION NUMBER: US 09/445,375
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
 0; Mismatches
 728; Conservative
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Pred. No. 2.9e-224;
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GENERAL INFORMATION: US20040131591A1
GENERAL INFORMATION:
APPLICANT: OKTARA Biomedica (UK) Ltd.
APPLICANT: Kingsman, Alan
APPLICANT: Garroll, Miles
APPLICANT: Hard, Fions
APPLICANT: Hard, Fions
APPLICANT: Hard, Fions
APPLICANT: Kingsman, Susan
APPLICANT: Hard, Fions
APPLICANT: Kingsman, Susan
APPLICANT: Hard, Fions
APPLICANT: Wyers, Kevin
APPLICANT: Wyers, Kevin
APPLICANT: Whers, Casolon
CURRENT PLING DATE: 2002-12-30
FRIOR APPLICATION NUMBER: US 10/060,585
PRIOR FILING DATE: 2002-11-23
PRIOR FILING DATE: 2000-11-13
PRIOR FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 40
SEQ ID NO 2
LENGTH : 1807
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SEQ ID NO 2
LENGTH: 1807
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ORGANISM: Artificial Sequence
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                                                                                               ; FEATURE:
; OTHER INFORMATION: Sequence encoding 5T4 single chain antibody
US-10-787-881A-2
PRIOR FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 1807
                                                                      TYPE: DNA ORGANISM: Artificial Sequence
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789 ATCAAACGG 797
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RESULT 7
US-10-060-585-3
Sequence 3, Application US/10060585; Publication No. US20030083290A1
GENERAL INFORMATION:

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99.4%; Score 724.4; DB 14;
Best Local Similarity 99.9%; Pred. No. 2.5e-223;
Matches 725; Conservative 0; Mismatches 1;
               APPLICANT: Bebbington, Christopher R. APPLICANT: Bebbington, Christopher R. APPLICANT: Carroll, Miles W. APPLICANT: Ellard, Fiona W. APPLICANT: Kingeman, Susan M. APPLICANT: Kingeman, Susan M. TITLE BOF INVENTION: VECTOR SYSTEM TITLE REPERENCE: DYOUZ: 0010CP1 CURRENT FILING DATE: 2002-09-06 CURRENT FILING DATE: 1998-06-04 PRIOR PLING DATE: 1997-06-04 PRIOR PLING DATE: 1997-06-04 PRIOR PLING DATE: 1997-06-04 PRIOR PLING DATE: 1997-06-04 PRIOR PLING DATE: 1997-06-07 PRIOR PLING DATE: 1997-06-07 PRIOR PLING DATE: 1997-06-07 PRIOR PLING DATE: 1997-06-20 PRIOR PLING DATE: 1997-07-04 PRIOR PLING DATE: 1997-07-04 PRIOR PLING DATE: 1997-07-04 PRIOR PLING DATE: 1997-07-04 PRIOR PLING DATE: 1997-07-04 PRIOR PLING DATE: 1999-11-18 PRIOR PLING DATE: 1999-11-18 VUMBER: PRIOR PLING DATE: 1999-11-18 VUMBER: PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PLING DATE: 2000-11-13 PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR P
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US-10-060-585-3
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Kingsman, Alan J.
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        301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA
                                     339 GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT
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                                                                                           361 GGTGGTGGTGGGGGGGGGGGGGGGCACTGGCGGCGGCGGATCTAGTATTGTGATGACC
                                                                                                                                                                          421 CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCC
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; OTHER INFORMATION: Sequence encoding fusion protein B7-1.5T4.1
US-10-787-881A-3
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Pred. No. 2.5e-223;
0; Mismatches 1;
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APPLICANT: Kingsman, Susan M.
APPLICANT: Kingsman, Susan M.
APPLICANT: Ellard, Fiona M.
APPLICANT: Ellard, Fiona M.
APPLICANT: Ellard, Fiona M.
APPLICANT: Myers, Kevin A.
TITLE OF INVENTION: Vector
FILE REFERENCE: 02191-000330US
CURRENT APPLICATION NUMBER: US/10/787,881A
CURRENT FILING DATE: 2004-02-25
PRIOR APPLICATION NUMBER: US 09/445,375
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 24
SEQ TRANKE: Patentin Version 3.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 3, Application US/10787881A; Publication No. US20050032216A1
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Best Local Similarity 99.9
Matches 725, Conservative
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1339. GGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTT
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99.4%; Score 724.4; DB 18; Length 1467;
Best Local Similarity 99.9%; Pred. No. 2.5e-223;
Matches 725; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kingeman, Alan
APPLICANT: Kingeman, Alan
APPLICANT: Garroll, Miles
APPLICANT: Earroll, Miles
APPLICANT: Earroll, Miles
APPLICANT: Elard, Fiona
APPLICANT: Elard, Fiona
APPLICANT: Kingeman, Susan
APPLICANT: Kingeman, Susan
APPLICANT: Myers, Kevin
APPLICANT: Myers, Kevin
APPLICANT: Lamikandra, Abigail
TITLE OF INVENTION: VECTOR SYSTEM
FILE REFRENCE: $32682000920,
CURRENT APPLICATION NUMBER: US 10/060,585
PRIOR PRILING DATE: 2002-12-29
PRIOR PLLING DATE: 2002-01-29
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 2000-01-13
PRIOR FILING DATE: 1908-06-04
NUMBER OF SEQ ID NOS: 40
SEQ ID NOS: 40
SEQ ID NOS: 40
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                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/10334235
Publication No. US20040131591A1
GENERAL INFORMATION:
APPLICANT: Oxfard Biomedica (UK) Ltd.
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ORGANISM: Artificial Sequence
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99.3%; Score 724.2; DB 14; Length
Best Local Similarity 99.6%; Pred. No. 2.9e-223;
Matches 726; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACCTGGTGAAGCCT
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pBSII/Leader/scFv/HGl.
US-10-104-522-5
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PUDLICATION NO. US20030018004A1
GENERAL INFORMATION:
APPLICANT: Ringsman, Susan M.
APPLICANT: Bebbington, C.R.
APPLICANT: Ellard, Fiona M.
APPLICANT: Ellard, Fiona M.
APPLICANT: Carroll, Miles W.
TITLE OF INVENTION: VECTOR
FILE REFERENCE: DYOUZ3.001DV1
CURRENT APPLICATION NUMBER: US/10/104,522
CURRENT FILING DATE: 2002-03-22
RIOR APPLICATION NUMBER: PCT/GB98/01627
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1999-06-04
PRIOR PLING DATE: 1997-06-04
PRIOR APPLICATION NUMBER: GB9711579.4
PRIOR PLING DATE: 1997-06-07
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Pred. No. 2.9e-223;
0; Mismatches 3;
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APPLICANT: Bebbington, Christopher
APPLICANT: Bebbington, Christopher
APPLICANT: Blazd, Flona
APPLICANT: Blazd, Flona
APPLICANT: Kingsman, Susan
APPLICANT: Kingsman, Susan
APPLICANT: Lamkkandra, Abigail
TITLE OF INVENTION: VECTOR SYSTEM
FILE REPERENCE: 53262000920
CURRENT PEPLICATION NUMBER: US/10/334,235
CURRENT FILING DATE: 2002-12-30
PRIOR APPLICATION NUMBER: US 10/060,585
PRIOR PILING DATE: 2000-11-13
PRIOR PILING DATE: 2000-11-13
PRIOR FILING DATE: 1998-06-04
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 1518
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                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Oxfard Biomedica (UK) Ltd
                                                                                                                                                                                                                                                                                     S-10-334-235-5
Sequence 5, Application US/10334235
Publication No. US20040131591A1
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ORGANISM: Artificial Sequence
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APPLICANT: Myers, Kevin A.
TITLE OF INVENTION: VBCTOR SYSTEM
FILE REPERENCE: DYOUZ3.001CP1
CURRENT APPLICATION NUMBER: US/10/060,585
CURRENT FILING DATE: 2002-09-06
PRIOR PELLING DATE: 1998-06-04
PRIOR FILING DATE: 1998-06-04
PRIOR FILING DATE: 1997-06-04
PRIOR FILING DATE: 1997-06-06
PRIOR FILING DATE: 1997-06-20
PRIOR FILING DATE: 1997-06-20
PRIOR FILING DATE: 1997-06-20
PRIOR FILING DATE: 1997-06-10
PRIOR FILING DATE: 1997-01-04
PRIOR FILING DATE: 1997-01-04
PRIOR FILING DATE: 1997-01-04
PRIOR FILING DATE: 1997-07-04
PRIOR FILING DATE: 1997-07-04
PRIOR FILING DATE: 1997-07-04
PRIOR FILING DATE: 1999-11-18
PRIOR FILING DATE: 1999-11-18
PRIOR SEQ ID NOS: 27
NUMBER OF SEQ ID NOS: 27
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: B7 link ScFv sequence US-10-060-585-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1518
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967 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGGCCTAC 1026
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181 AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGGCCTAC
                                                                                    241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGGTCTATTACTGTGCAAGATCTACT
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| APPLICANT: Oxfard Blomedica (UK) Ltd.
| APPLICANT: Kingsman, Alan
| APPLICANT: Ringsman, Alan
| APPLICANT: Bebbington, Christopher
| APPLICANT: Bebbington, Christopher
| APPLICANT: Bebbington, Miles
| APPLICANT: Ellard, Fiona
| APPLICANT: Kingsman, Susan
| APPLICANT: Kingsman, Susan
| APPLICANT: Kingsman, Susan
| APPLICANT: Lamikandra, Abigail
| TITLE OF INVENTION: VECTOR SYSTEM
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| TITLE OF INVENTION: VECTOR SYSTEM
| VECTOR STATION NUMBER: US 09/445,375
| PRIOR FILING DATE: 1998-06-04
| NUMBER OF SEQ ID NOS: 40
| SEQ ID NO 16
| LENGTH: 9100
| TYPE: DNA
| ORGANISM: Artificial Sequence
| FEATURE:
| TYPE: DNA
| OTHER INFORMATION: plasmid
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99.3%; Score 724.2; DB 19;
Best Local Similarity 99.6%; Pred. No. 2.9e-223;
Matches 726; Conservative 0; Mismatches 3; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Sequence encoding B7 Link scFv
US-10-787-881A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOSTICANT SECULAR SECTION NO. 105.1078781A

SEQUENCE INFORMATION:
GENERAL INFORMATION:
APPLICANT: OXIOT BIOMEDICA (UK) Ltd.
APPLICANT: Ringsman, Susan M.
APPLICANT: Bebbington, Christopher R.
APPLICANT: Bebbington, Christopher R.
APPLICANT: Ellard, Fiona M.
APPLICANT: Garroll, Miles W.
APPLICANT: Myers, Kevin A.
ITTLE OF INVENTION: Vector
FILE REFERENCE: 021911-000330US
CURRENT APPLICATION NUMBER: US/10/787,881A
CURRENT FILING DATE: 2004-02-25
PRIOR APPLICATION NUMBER: PCT/GB98/01627
PRIOR APPLICATION NUMBER: PCT/GB98/01627
PRIOR APPLICATION NUMBER: PCT/GB98/01627
PRIOR SEQ ID NOS: 24
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial Sequence
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|507 ATCAAACGG 1515
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                                                          1 GAGGTCCAGCTTCAGCAGTCTGGACCTGACGTGAAGCCTGGGGGCTTCAGTGAAGATA
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                                        Gaps
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                    Length 9100;
                                        4; Indels
                   DB 18;
                  99.1%; Score 722.6; DB 18
99.5%; Pred. No. 2.1e-222;
tive 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6, Application US/10104522;
Publication No. US20030018004A1
GENERAL INFORMATION;
APPLICANT: Kingsman, Susan M.
APPLICANT: Elbard, Fions M.
APPLICANT: Ellard, Fions M.
TITLE OF INVENTION: VECTOR
CURRENT APPLICATION NUMBER: US/10/104,522;
CURRENT APPLICATION NUMBER: 09/445375;
PRIOR APPLICATION NUMBER: 09/445375
                                      Matches 725; Conservative
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                            Similarity
US-10-334-235-16
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US-10-104-522-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACTTCAGTCACGGCTCTTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAGACTCCCACATTCCTGCTTGTTTCAGCAGGAGAGGGTTACCATAACCTGCAAGGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     549 AGTCAGAGTGTGAGTAATGATGATGTTGGTTGGTACCAACAGAAGGCAGGGCAGGGCACTCCTACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GAGGICCAGCITCAGCAGICTGGACCTGACCTGGTGAAGCCTGGGGGCTTCAGTGAAGATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGGTCTATTACTGTGCAAGATCTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA
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; OTHER INFORMATION: 5T4 scFv-human IgE fusion construct.
US-10-104-522-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 98.9%; Score 721; DB 14;
Best Local Similarity 99.3%; Pred. No. 3.6e-222;
Matches 724; Conservative 0; Mismatches 5;
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: PCT/GB98/01627
PRIOR PLING DATE: 1998-06-04
PRIOR PILING DATE: 1998-06-04
PRIOR FILING DATE: 1997-06-04
PRIOR FILING DATE: 1997-06-04
PRIOR FILING DATE: 1997-06-20
PRIOR PILING DATE: 1997-06-20
PRIOR APPLICATION NUMBER: GB9714230.1
PRIOR APPLICATION NUMBER: GB9714230.1
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FREESEQ FOR WINDOWS Version 4.0
LENGTH: 2090
                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
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789 ATCAAACGG 797

Search completed: March 15, 2005, 00:12:29 Job time : 577 secs

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Title: Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Searched:

Database

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Silva, W.A. Jr.

Silva, W.A. Jr.

Open reading frame ESTB - an efficient strategy for analysis of the honey beet transcriptome

Unpublished (2004)

Contact: Silva Jr. W. A.

Molecular Genetics and Bioinformatics Laboratory

Departament of Genetics, FWRP/USP, FUNDHERP

Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil

Tel: +55 16 3963300

Fax: +55 16 3963300

Fax: +55 16 3963300

Fax: +55 16 3963300

Fax: +55 16 3963300

Fax: High quality sequence as derived from the FAPESP Genome Program

High quality sequence stori: 66

High quality sequence stori: 65

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Apidae, Apis.

1 (bases 1 to 872)

Nunes, F.M.F., Valente, V., Sousa, J.F., Cunha, M.A.V., Pinheiro, D.G.,
Maia, R.M., Araujo, D.D., Costa, M.C.R., Martins, W.K., Carvalho, A.F.,
Monesi, N., Nascimento, A.M., Peixoto, P.M.V., Silva, M.F.R.,
Ramoss, R.G.F., Reis, L.F.L., Dias Neto, E., Souza, S.J., Simpson, A.J.G.,
Eago, M.A., Soares, A.E.F., Bitondi, M.M.G., Espreafico, E.M.,
Espindola, F.S., Paco-Larson, M.L., Simoes, Z.L.P., Hartfelder, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eŭkaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CK629396
AMO-AA0013-110902-011-H03 AA0013 Apis mellifera CDNA, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 7; Length 872;
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/sex="female, worker"
/dev_stage="adult"
/clone_lib="AA0013"
/note="Organ: whole body"
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/mol_type="mRNA"
/strain="Africanized"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39.9%; Score 291;
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BH121432
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1. .872
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KEYWORDS
SOURCE
ORGANISM
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CK629396/c
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DEFINITION
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AM1-AA001
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AGENCOURT
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AM3-AP001
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AM0-AM000
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                                                                                                                            March 14, 2005, 18:20:07; Search time 3220 Seconds (without alignments) 8617.656 Million cell updates/sec
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CAS78686 K
CK632348 A
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BU523606
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BX969451
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Compugen Ltd.
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                    version :
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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729
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6011
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EST 26-MAR-2004

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Apis mellifera
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Hymenoptera, Apocrita, Aculeata, Apoidea,
Apidae, Apis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCCACCAAGCTGGAAATCAAAC 727
                                                                                                                                                                                                                                                                                                           420 GGCGCTACTTT---GACTTGTGGGGCCAAGGGACCACGGTCACCGTCTCCTCATGTGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                   248 TCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTATGATTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        363 GCGGTTCAGGCGGAGGTGGCTCTGGCGGTGGCGGGATCTGACATTGAGCTCACCCAGTCTC
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                                                                                                                                                                                                                                                                                     128 AGAGCCTIGAGIGGATIGGACGIATIAATCCTAACAAIGGIGTTACICTCTACAACCAGA
                                                                                                                                                                                                                                                                                                                                                             188 AATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACATGGAGC
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AM2-AA0023-091202-021-F02 AA0023 Apis mellifera cDNA, mRNA
                                                                                                                                                                                                                                                    . 9
                                                                                                                                                                                                                 Length 601;
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                                                                                                                                         cDNA"
                                                                                                                                                                                                               DB 5;
                                                                                                                                                                                                            39.0%; Score 284.4; DB 5;
llarity 69.3%; Pred. No. 1.4e-74;
Conservative 1; Mismatches 178;
                                                                             /mol_type="mRNA"
/db_xref="taxon:118799"
/clone="carabus4912"
/clone_lib="carabus granulatus /note="Vector: pUC18"
                                            1. .601
/organism="Carabus granulatus"
                         Location/Qualifiers
         Email: p.foster@nhm.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CK629846
CK629846.1 GI:45754321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    601 bp mRNA linear EST 30-NOV-2002 carabus4912.b Carabus granulatus cDNA Carabus granulatus cDNA clone carabus4912 5', mRNA sequence.
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Carabus granulatus
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Bukaryota, Endopterygota; Coleoptera; Adephaga; Carabidae; Carabini,
Carabina, Carabus; Carabus.
1 (bases 1 to 601)
Theodorides, K., de Riva, A., Gomez-Zurita, J., Foster, P.G. and
                                                            136
                                                                                                                                                                                                             256
                                                                                                                                AGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTACAACCAGAAATTCAAGG 196
                                                                                                                                                                         634
                                                                                                                                                                                                                                                                                                   376
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                                                                                                                                                                                                                                                                                TGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACTATGATTACGAACTATG 316
                                                                                                                                                                                                                                                                                                                                                                                     TT---GACTIGGGNCCAAGGGACCACGTCACCGTCTCCATGTGGAGNCGGTTCAG 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 ATTCTCTCACAATCAACGAATGCAGGCTGAGGATGCTGCCACTTATTACTGCCAGGAGT 160
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                                                        GTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCGAGAGCCATGGAAAGAGCCTTG
                                                                                         GCTACATCTTCACAAGTTATGATATAGACTGGGTGAGGCAGACGCCTGAACAGGGACTTG
                                                                                                                                                                   AGTGGATTGGATGTTTT-TCCTGGAGAGGGGAGTACTGAATACAATGAGAAGTTCAAGG
                                                                                                                                                                                                          ACAAGGCCATATTAACTGTAGACAAGTCATCCACCACGAGCCTACATGGAGCTCCGCAGCC
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                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          159 GGAGTGGTTATCCGTACGTTCGGAGGGGGGCACCAAGCTGGAGCTGAAACGG 107
                       7;
                     Indels
 Pred. No. 1.6e-76;
1; Mismatches 199;
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Vogler, Entomology
The Natural History Museum
Cromwell Road, London, SW7
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BQ474958.1 GI:25957232
68.3%;
Best Local Similarity 68.3
Matches 446; Conservative
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Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                             BQ921928
BQ921928.1 GI:22336959
EST.
                                                                                                                                 CGG 729
                                                                                                                                                        CGG 91
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Nunes, F.M.F., Valente, V., Sousa, J.F., Cunha, M.A.V., Pinheiro, D.G., Maia, R.M., Araujo, D.D., Costa, M.C.R., Martins, W.K., Carvalho, A.F., Monesi, N., Araujo, D.D., Costa, M.C.R., Martins, W.K., Carvalho, A.F., Monesi, N., Nascimento, A.M., Peixoto, P.M.V., Silva, M.F.R., Ramos, R.G.P., Reis, L.F.L, Dias Neto, E., Souza, S.J., Simpson, A.J.G., Eago, M.A., Soares, A.E.E., Btondi, M.M.G., Espreafico, E.M., Espindola, F.S., Paco-Larson, M.L., Simoes, Z.L.P., Hartfelder, K. and Silva, W.A. Jr.
Open reading frame ESTs - an efficient strategy for analysis of the honey bee transcriptome
Unpublished (2004)
Contact: Silva Jr. W. A.
Molecular Genetics, FWRPUSP, FUNDHERP
Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil
Tel: +5516 39633309
Email: wilsonjr@usp.br
This sequence start: 64
High quality sequence start: 64
High quality sequence store: 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTACATGGAG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGTICAAGGGCAGGCCAACACTGAGTGTAGACAAGTCCTCCCAGCACAGCCTATATGGAG 568
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       307 ACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCAGGTGGT 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCACATTCCTGCTTGTTTCAGCAGGAGACAGGGTTACCATAACCTGCAAGGCCAGTCAG 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   389 CCAGCAATCATGTCTGCATCTCCAGGGGAGAGGGTCACCATGACCTGCAGTGCCAGCTCA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTGTGAGTAATGATGTAGDTTGGTACCAACAGAGGCCAGGGCAGTCTCCTACACTGCTC 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGTATACG----TTACATATATTGGTACCAACAGAAGCCTGGATCCTCCCCCAGACTCCTG 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 272 ATTTATGACACCATCCAACGTGGCTCCTGGAGTCCCTTTTCGCTTCAGTGGCAGTGGGTTT 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 283.4; DB 7;
Pred. No. 3.5e-74;
1; Mismatches 203;
                                                                                                                                                                                                                                                                                                                                                                             /organism="Apis mellifera"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="AA0023"
/note="Organ: whole body"
                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/strain="Africanized"
                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:7460"
/sex="female, worker"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 452; Conservative
                                                                                                                                                                                                                                                                                                                                                              j. .1104
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BO921928 1010 bp mRNA linear EST 20-AUG-2002 AGENCOURT 8952829 NCI CGAP CO24 Mus musculus cDNA clone IMAGE:6475284 5', mRNA sequence.
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/clone="Dublob Repeated Resistant" |
/clone lib="NUI CGAP CO24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
/site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTAC 180
                                                           212 gegicercitarreferekanteanegantegageteganegareerekeenetraktak 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: The Copko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lln.gov
Plate: LLAM14013 row: m column: 13
High quality sequence stop: 608.
                                                                                                                                                                            152 TGCCAGGAGTGGAGTGGTTATCCGTACACGTTCGGAGG-GGGACCAAGCTGGAGCTGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGGTCCAGCTCCAGCAGTCTGGACCTGAGATGGTGAAGCCTGGGGCTTCAGTGAAGATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189 CATGGAAAGCGCCTTGAGTGGATTGGACGTGTTAATCCTAATAATGGTGAAAGTAGGTAT
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607 GGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCTGAAGACCTGGCAGTTTATTTC
                                                                                                                                         TGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGAGGCACCCAAGCTGGAAATCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .1010
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'db xref="taxon:10090"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. B. 1 (bases 1 to 724)

E 1 (bases 1 to 724)

NIH-MCC http://mgc.nci.nih.gov/.

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.lln.gov
Plate: LLAM9265 row: h column: 04

High quality sequence stop: 661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            BF168514 724 bp mRNA linear EST 30-OCT-2000 collaboration NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:4017075 5',
                                                                            645
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287 GAAGACCTGGCATTTTATTTCTGTCAGCAGGATTATAGCTCTCCGTACAGGTTCGGAGG 346
                                                                                                                                                                              646 GAAGACCIGGCAGITIAITICIGICAGCAAGAITATAATICICCICCGACGITCGGIGGA 705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="NCI_CGAP_Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
                                                                                                    227 CGCTTCACTGGCAGTGGATATGGGACGGATTTCACTTTTCACCATCACCACTGTGCAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TCCTGCAAGGCTTCTGGTTACTCATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC
                                                                          586 CGCTTCATTGGCAGTGGATATGGGACGGATTTCACTTTCACCATCAGCACTTTGCAGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .724
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="IMAGE:4017075"
                                                                                                                                                                                                                                                                                706 GGCACCAAGCTGGAAATCAAACGG 729
                                                                                                                                                                                                                                                                                                                               347 GGGACCAAGCTGGAAATAAAACGG 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
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TITLE
JOURNAL
COMMENT
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BF168514
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                                               241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
                                                                                                                                                                           369 AGGATCGGAGATTACTATGCTATGGACTACTAGGGGTCAAGGAACCTCAGTCACCGTCTCC 428
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/note="Organ: mammary; Vector: pCMV-SPORT6; Site 1: Sal1;
Site 2: Not1; Cloned unidirectionally. Primer: Öligo dT.
Library constructed by Life Technologies. Investigators
providing samples: Lothar Hennighausen/Robin Humphreys,
NIH"
AACCAGAAGTCCGAGGGCAAGGCCACATTGACTGTTGACAAATCCTCCACCACAGCCTAC 308
                                                                                                                                                 ATGAL --- TACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACGTCTCC 357
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                               Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
column: 12
High quality sequence stop: 591.
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Pred. No. 1.8e-73;
0; Mismatches 27; Indels 0
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/dev stage="7" months"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                            BE309592 594 bp mRNA 601094848F1 NCI_CGAP_Mam5 Mus musculus c
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/strain="mix FVB/N, C57BL/6J"
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Mus musculus
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BE309592
BE309592.1 GI:9168025
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Best Local Similarity 91.7%;
Matches 297; Conservative
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/db xref="taxon:10090"
/clone="IMAGE:3660374"
/tissue type="tumor, metastatic to mammary"
/lab_host="PH10B"
/clone lib="NOI CGAP Lu30"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: Sall; transgenic model NNT-1, expression driven by MMTV-ITR enhancer; Cloned unidirectionally. Primer: Oligo MMTV-ITR enhancer; Cloned unidirectionally. Primer: Oligo MTT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BF015548 507 bp mRNA linear EST 29-DEC-2000 uy23a08.yl NCI CGAP_Lu30 Mus musculus cDNA clone IMAGE:3660374 5' similar to SW:HV14_MOUSE P01758 IG HEAVY CHAIN V REGION 108A
                        recrecaagecriciggriacrearreacrescraciacracacecrescressina 218
                                                                           CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTAC 180
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                   AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC
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/organism="Mus musculus"
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High quality sequence stop: 4
Location/Qualifiers
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AACCAGAAATTCAAGGACAAGGCCATATTAACTGTAGACAAGTCATCCACCACAGCCTAC 240
                                                                                                                 275 AACCAGAAGTTCAAGGGCAAGGCCACATTGACTGTAGACAAATTCCTCCAGCACGCCTAC 334
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National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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/lab_host="DH10B"
/clone lib="NCI CGAP_Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NorI; Cloned unidarectionally. Primer: Oligo dr. Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Rolert Strausberg, Ph.D.

Email: cgapbs-remail.nh.gov

Email: cgapbs-remail.nh.gov

Tissue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:

http://image.llnl.gov

Plate: LiAM9265 row* k column: 04

High quality sequence stop: 678.
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/mol_type="mRNA"
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602093730F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4208022 5', BF580610
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Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                          703 GGTGAAGCAGACGCCTGNACAG-GACTTGAGTGGATTGGATG-ATTTTTCCTGGAGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                645 ANGTACTGAATACAATGAGAAGTTCAAGGGCAGGCACACACTGAGTGTAGACAAGTCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              408 TATTGTGATGACCCAGACTCCCACATTCCTGCTTGTTTCAGCAGACAGGGTTACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 408 CATTGAGCTCACCCAGTCTCCAGCAATCATGTCTGCATCTCCAGGGGAGAGAGGGGTCACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                468 AACCTGCAAGGCCAGTCAGAGTGTGAGTAATGATGTAGDTTGGTACCAACAGAAGCCAGG
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
1 (bases 1 to 883)
NHH-MGC http://mg.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                             Length 1419;
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                                                                                                                                                                                             Score 269.4; DB 7;
Pred. No. 6.7e-70;
1; Mismatches 185;
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green,
/dev_stage="adult"
/clone_lib="AA0014"
/note="Organ: whole body"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             708 CACCAAGCTGGAAATCAAACG 728
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68.8%;
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Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Apidae; Apis.
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                                                                                                                                                                                                                                                                                                                    TCCTGCAAGGCTTCTGGATACACATTCACTGGCTACTACATGCACTGGGTGAAGCAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC
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High quality sequence start: 63
High quality sequence stop: 605.
                                           Indels
Pred. No. 3.2e-70;
0; Mismatches 50;
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/strain="Africanized"
/db_xref="taxon:7460"
/sex="female, worker"
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Apis mellifera
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Fax: +55 16 39639309
Email: wilsonjr@usp.br
85.58;
                                           313; Conservative
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CK629414/c
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DEFINITION
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  585
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309
                                                                                                                                                                                                                                                   /db.xeref="taxxon:10090"
/db.xeref="taxxon:10090"
/clone="INAGE:4208022"
/dab.host="DH10B (Tl phage-resistant)",
/clone lib="NCI CGAP CO24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Not1;
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1 Not1;
/site_2: Sall; cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 GAAGACCTGGCAGTTTATTTCTGTCAGGATTATAGCTCTCCTCGGACGTTCGGTGGA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           250 CGCTTCACTGGCAGTGGACATGGGACGGATTTCACTTTCACCATCAGCTGTGCAGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        526 GGGCAGTCTCCTACACTGCTCATATCCTATACATCCAGTCGCTACGCTGGAGTCCCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGACCTGGCAGTTTATTTCTGTCAGCAAGATTATAATTCTCCTCCGACGTTCGGTGGA
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9771 row: 1 column: 07
High quality sequence stop: 639.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: The Cepko Laboratory
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.8%; Score 268; DB 2; Length 883; 93.2%; Pred. No. 1.5e-69; ive 0; Mismatches 20; Indels
                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCACCAAGCTGGAAATCAAACGG 729
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Matches 302; Conservative
                                                                                                                                                                           1. .883
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KEYWORDS
SOURCE
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JOURNAL
COMMENT
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AUTHORS
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BU523606
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скь29414
AMI-AA0014-041102-021-D05 AA0014 Apis mellifera cDNA, mRNA
sequence.
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Nunes, F.M.F., Valente, V., Sousa, J.F., Cunha, M.A.V., Pinheiro, D.G., Maia, R.M., Araujo, D.D., Costa, M.C.R., Martins, W.K., Carvalho, A.F., Monesi, N., Nascimento, A.M., Peixoto, P.M.V., Sllva, M.F.R., Ramos, R.G.P., Rels, L.F.L., Dias Neto, E., Souza, S.J., Simpson, A.J.G., Zago, M.A., Soares, A.E.E., Bitondi, M.M.G., Espreafico, E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180
                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="IMAGE:6530296"
/lab_host=="NGIO (CAP_CO34"
/clone="lorgan: colon; Vector: pCWV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240
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Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277 AACCAGAAGTTCAAGGACAAGGCCACATTGACTGTAGACAAACCCTCCAGGACAGGCTTC 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCGGTCTATTACTGTGCAAGATCTACT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              397 TATGATIC---CTATGCTATGGACTACTGGGGGTCAAGGAACCTCAGTCACCGCTCTCCTCA 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 gaggiccagciacaacaarcigaaccigagciggaagcigaagciggggcircagrgaagarg 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 ATGATTACGAACTATGTTATGGACTACTGGGGTCAAGTAACCTCAGTCACCGTCTCCTCA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATGGAAAGAGCCTTGAGTGGATTGGACGTATTAATCCTAACAATGGTGTTACTCTCTAC
                                     ре
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DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.B. Consortium/LLNL at: http://mage.llnl.gov
Plate: LLAM14111 row: m column: 16
High quality sequence stop: 582.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 931;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.6%; Score 266.6; DB 5;
llarity 85.6%; Pred. No. 4.1e-69;
Conservative 0; Mismatches 49;
                                                                                                                                                                                                                                                                    /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
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CK629414.1 GI:45753889
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BI104341 598 bp mRNA linear EST 26-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332 ATGGAGCTCCGCAGCCTGACATCTGAGGACTCTGCAGTCTATTACTGTGCAAGATCGATG 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="NCI_CGAP_Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: Sall;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue type="spontaneous tumor, metastatic to mammary.
Stem coll origin."
/lab host="DR108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272 AACCAGAAGTICAAGGGCAAGAGCCACATIGACIGTAGAAAAGTCCICCAGCACAGCCTAC
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                  127 ACACGTTCGGAGGGGGGACCAAGCTGGAGCTGAAACGG 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
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Pred. No. 2.9e-68;
0; Mismatches 49
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organism="Mus musculus"
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clone="IMAGE:5035013"
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/strain="CZECH II"
                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                 BI104341
BI104341.1 GI:14555234
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Best Local Similarity 84.3
Matches 312; Conservative
                                                                                                                                                                                                                     mRNA sequence.
                                                                                                                                                                                                                                                                                                           EST.
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Espindola, F.S., Paco-Larson, M.L., Simoes, Z.L.P., Hartfelder, K. and Silva, W.A. Jr.
Open reading frame ESTs - an efficient strategy for analysis of the honey bee transcriptome
L. Unpublished (2004)
Conteact: Silva Jr. W. A.
Molecular Genetic and Bioinformatics Laboratory
Departament of Genetics, FWRP/USP, FUNDHERP
Rua Tenente Catao Roxo, 2501, CEP 14051-140, Brazil
Tel: +55 16 3963300
Fax: +55 16 3963300
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1; Mismatches 198; Indels 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Apis mellifera"
/mol_type="mRNA"
/strāln="Africanized"
/db_xref="taxon:7460"
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/dev stage="adult"
/clone_lib="AA0014"
/note="Organ: whole body"
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Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Direct Submission
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Mus musculus
Mus musculus
Mukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mu
   392 GGGTTACGGGGGTGGGGCCCCTACTACTTTGACTACTGGGGCCAAGGCACCACTATCACA 451
                                                                                                                                                                                                                                                                             BX969451

Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN79016, genomic survey sequence.

BX969451
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35.9%; Score 262; DB 9; Length 842;
Best Local Similarity 93.2%; Pred. No. 9.9e-68;
Matches 274; Conservative 0; Mismatches 20: Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSS; genome survey sequence; MICER.
Mus musculus (house mouse)
Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        BX969451.1 GI:49700874
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                                                                     352 GTCTCCTCAG 361
                                                                                                       mRNA sequence.
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
/db_xref="taxon:10090"
/db_not="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Type="Typ
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NIH-WGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey B. Green, M.D.
CONA Library Preparation: Life Technologies, Inc.
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9767 row: n column: 13
High quality sequence stop: 672.
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35.8%; Score 261; DB 2;
Best Local Similarity 85.0%; Pred. No. 1.9e-67;
Matches 307; Conservative 0; Mismatches 45;
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